

GenCore version 5.1.1.6  
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OM protein - protein search, using sw model

Run on: January 20, 2004, 13:54:52 ; Search time 21 Seconds  
(without alignments)  
27.477 Million cell updates/sec

Title: US-09-919-703-1

Perfect score: 30

Sequence: 1 SVDVEY 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 75 summaries

Database : PIR 76:\*

1: p1r1:\*

2: p1r2:\*

3: p1r3:\*

4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	30	100.0	128	2 S77671	streptokinase A (E
2	30	100.0	157	2 AH3460	arsenate reductase
3	30	100.0	279	2 T09620	probable lectin 2
4	30	100.0	415	1 B250	streptokinase (BC
5	30	100.0	440	1 A22801	streptokinase prec
6	30	100.0	440	2 S02723	streptokinase G pr
7	30	100.0	440	2 S02724	streptokinase A pr
8	30	100.0	1274	2 T10729	transferrin-like p
9	29	96.7	186	2 T31951	hypothetical prote
10	29	96.7	215	2 C97297	probable phosphata
11	29	96.7	1207	2 T16011	hypothetical prote
12	29	96.7	1595	2 T31082	endo-1,4-beta-xyla
13	28	93.3	311	1 I0R544	primosome componen
14	28	93.3	629	2 T27619	hypothetical prote
15	27	90.0	50	2 A60745	major outer membra
16	27	90.0	180	2 C84465	protein B0244.9 [i
17	27	90.0	271	2 G90898	probable tail fibe
18	27	90.0	271	2 B85842	hypothetical prote
19	27	90.0	368	2 JN0848	outer membrane 40K
20	27	90.0	368	2 S46435	porin precursor -
21	27	90.0	371	2 S46436	porin foma precurs
22	27	90.0	375	2 G85631	hypothetical prote
23	27	90.0	391	2 S61704	probable transcrip
24	27	90.0	399	2 E70598	probable pPE prote
25	27	90.0	401	1 QX8P1L	hypothetical prote
26	27	90.0	407	2 G90907	probable tail fibe
27	27	90.0	437	2 E90968	probable tail fibe
28	27	90.0	437	2 E90996	probable tail fibe
29	27	90.0	437	2 H90854	probable tail fibe

ALIGNMENTS

RESULT 1

S77671  
Streptokinase A (EC 3.4.-.-) (alleles 2 and 3) - Streptococcus pyogenes (fragment)  
C:Species: Streptococcus pyogenes  
C:Date: 24-Jul-1998 #sequence\_revision 24-Jul-1998 #text\_change 22-Jun-1999  
C:Accession: S77671; S77672  
R:Kapoor, V.; Kanjilal, S.; Hamrick, M.R.; Li, L.L.; Whittam, T.S.; Sawyer, S.A.; Musser  
Mol. Microbiol. 16, 509-519, 1995  
A:Title: Molecular population genetic analysis of the streptokinase gene of Streptococ  
A:Reference number: S77671; MUID:96037795; EUID:7565111  
A:Accession: S77671  
A:Status: translation not shown  
A:Molecule type: DNA  
A:Residues: 1-128 <KAP>  
A:Cross-references: EMBL:U25853; NID:g818908; PIDN:AAA85729.1; PID:g818909  
A:Experimental source: strain ET1/W1  
A:Note: allele 2  
A:Accession: S77672  
A:Status: translation not shown  
A:Molecule type: DNA  
A:Residues: 1-128 <KA2>  
A:Cross-references: EMBL:U25854; NID:g818910; PIDN:AAA85730.1; PID:g818911

30	27	90.0	438	2 D90734	probable tail fibe
31	27	90.0	439	2 C90769	probable tail fibe
32	27	90.0	439	2 B85816	probable tail fibe
33	27	90.0	439	2 A85719	probable tail fibe
34	27	90.0	439	2 A85741	hypothetical prote
35	27	90.0	440	2 F85584	probable tail comp
36	27	90.0	621	2 H81971	probable ABC trans
37	27	90.0	621	2 C81026	ABC transporter, A
38	27	90.0	831	2 E96830	hypothetical prote
39	27	90.0	864	2 JC4624	alpha-glucosidase
40	27	90.0	971	2 B90835	probable tail fibe
41	27	90.0	973	2 C85693	probable membrane
42	27	90.0	1077	2 D90387	peptidase related
43	27	90.0	1122	2 G64887	probable tail fibe
44	27	90.0	1471	1 S30790	myosin MYO4 - yeas
45	27	90.0	3344	2 JQ1899	genome polyprotein
46	26	86.7	47	2 F90945	hypothetical prote
47	26	86.7	47	2 A85794	hypothetical prote
48	26	86.7	47	2 H64943	hypothetical prote
49	26	86.7	47	2 AF0727	conserved hypotet
50	26	86.7	93	2 T08801	hypothetical prote
51	26	86.7	130	2 T49629	related to finger
52	26	86.7	140	2 G86413	F28N24.17 protein
53	26	86.7	148	2 H64025	hypothetical prote
54	26	86.7	155	2 D89900	conserved hypotet
55	26	86.7	155	2 F90262	conserved hypotet
56	26	86.7	191	2 E70042	hypothetical prote
57	26	86.7	197	2 AC0033	conserved hypotet
58	26	86.7	216	2 T44352	hypothetical prote
59	26	86.7	244	2 A83236	hypothetical prote
60	26	86.7	263	2 T47536	hypothetical prote
61	26	86.7	264	2 AH376	iron(III) dicitrat
62	26	86.7	270	2 B86486	protein F2809.7 [i
63	26	86.7	275	2 E83655	signal peptidase-1
64	26	86.7	284	2 S68216	phosphoprotein pho
65	26	86.7	287	2 C59304	methylinviologen-red
66	26	86.7	301	2 T33936	hypothetical prote
67	26	86.7	303	2 T13598	typsin homolog -
68	26	86.7	303	2 JQ1382	hypothetical 34K p
69	26	86.7	305	2 F72456	hydroxymethylbilan
70	26	86.7	307	2 S73632	Holliday junction
71	26	86.7	307	2 G64239	Holliday junction
72	26	86.7	319	2 AD2645	flagellar motor sw
73	26	86.7	321	2 D97427	flagellar motor sw
74	26	86.7	326	1 QGVZML	T2 protein - myxom
75	26	86.7	343	2 A81529	hypothetical prote

A;Experimental source: strain E2/M3  
A;Note: allele 3  
C;Genetics:  
A;Gene: ska  
C;Superfamily: streptokinase  
C;Keywords: hydrolase; plasminogen activator; virulence

Query Match 100.0%; Score 30; DB 2; Length 128;  
Best Local Similarity 100.0%; Pred. No. 7;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVEY 6  
|||||  
Db 17 SVDVEY 22

## RESULT 2

AH3460  
arsenate reductase [imported] - Brucella melitensis (strain 16M)  
C;Species: Brucella melitensis  
C;Date: 01-Feb-2002 #sequence\_revision 01-Feb-2002 #text\_change 01-Feb-2002  
C;Accession: AH3460  
R;DelVecchio, V.G.; Kapral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova,  
; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess  
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002  
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitensis  
A;Reference number: AD3252; PMID:11756688  
A;Accession: AH3460  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-157 <KUR>  
A;Cross-references: GB:AE008917; PIDN:AAL52851.1; PID:G17983693; GSPDB:GN00190  
A;Experimental source: strain 16M  
C;Genetics:  
A;Gene: BME11670  
A;Map position: I

Query Match 100.0%; Score 30; DB 2; Length 157;  
Best Local Similarity 100.0%; Pred. No. 8;8;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVEY 6  
|||||  
Db 114 SVDVEY 119

## RESULT 3

T09620  
probable lectin 2 precursor - alfalfa  
C;Species: Medicago sativa (alfalfa)  
C;Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 20-Jun-2000  
C;Accession: T09620  
R;Brill, L.M.; Pieterneel, V.R.  
submitted to the EMBL Data Library, March 1998  
A;Description: Legume seed lectin genes: sequence of Mslec2 from Alfalfa, Alfalfa and Sw  
A;Reference number: Z16780  
A;Accession: T09620  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: DNA  
A;Residues: 1-279 <BRI>  
A;Cross-references: EMBL:Y16754  
A;Experimental source: cultivar Chief  
C;Genetics:  
A;Gene: lec2  
C;Superfamily: plant lectin  
C;Keywords: calcium; glycoprotein; lectin  
F;1-25/Domain: signal sequence #status predicted <SIG>  
F;26-279/Product: probable lectin 2 #status predicted <MAT>

Query Match 100.0%; Score 30; DB 2; Length 279;  
Best Local Similarity 100.0%; Pred. No. 17;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVEY 6  
|||||  
Db 208 SVDVEY 113

## RESULT 4

BZSO  
streptokinase (EC 3.4.-.-) - Streptococcus sp.  
C;Species: Streptococcus sp.  
C;Date: 05-Apr-1983 #sequence\_revision 05-Apr-1983 #text\_change 23-Aug-1996  
C;Accession: A00967  
R;Jackson, K.W.; Tang, J.  
Biochemistry 21, 6620-6625, 1982  
A;Title: Complete amino acid sequence of streptokinase and its homology with serine pro  
A;Reference number: A00967; MUID:83127125; PMID:6760891  
A;Accession: A00967  
A;Molecule type: protein  
A;Residues: 1-415 <JAC>  
A;Note: 169-Asp and 181-Asp were also found  
A;Note: this protein is not a protease, but it activates plasminogen by complexing with  
C;Superfamily: streptokinase  
C;Keywords: hydrolase

Query Match 100.0%; Score 30; DB 1; Length 415;  
Best Local Similarity 100.0%; Pred. No. 26;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVEY 6  
|||||  
Db 157 SVDVEY 162

## RESULT 5

Az2801  
streptokinase precursor - Streptococcus "equisimilis"  
C;Species: Streptococcus "equisimilis"  
C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 24-Sep-1999  
C;Accession: A22801  
R;Malke, H.; Roe, B.; Ferretti, J.J.  
Gene 34, 357-362, 1985  
A;Title: Nucleotide sequence of the streptokinase gene from Streptococcus equisimilis H  
A;Reference number: A22801; MUID:85232082; PMID:2989113  
A;Accession: A22801  
A;Molecule type: DNA  
A;Residues: 1-440 <MAL>  
A;Cross-references: GB:X72832; NID:G407876; PIDN:CAAS1351.1; PID:G407879  
A;Experimental source: strain H46A  
C;Genetics:  
A;Gene: skc  
C;Superfamily: streptokinase

Query Match 100.0%; Score 30; DB 1; Length 440;  
Best Local Similarity 100.0%; Pred. No. 28;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVEY 6  
|||||  
Db 183 SVDVEY 188

## RESULT 6

S02723  
streptokinase G precursor - Streptococcus sp. (strain 19908)  
C;Species: Streptococcus sp.  
C;Date: 01-Dec-1989 #sequence\_revision 01-Dec-1989 #text\_change 22-Jun-1999  
C;Accession: S02723  
R;Walter, F.; Siegel, M.; Malke, H.  
Nucleic Acids Res. 17, 1262, 1989  
A;Title: Nucleotide sequence of the streptokinase gene from a group-G Streptococcus.  
A;Reference number: S02723; MUID:89160265; PMID:2922269  
A;Accession: S02723  
A;Molecule type: DNA  
A;Residues: 1-440 <WAL>

A:Cross-references: EMBL:X13400; NID:G47095; PIDN:CAA31766.1; PID:G47096

C:Genetics:

A:Gene: skg

C:Superfamily: streptokinase

F:1-26/Domain: signal sequence #status predicted <SIG>

F:27-440/Product: streptokinase #status predicted <MAT>

Query Match 100.0%; Score 30; DB 2; Length 440;

Best Local Similarity 100.0%; Pred. No. 28;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVDVEY 6

|||||

Db 183 SVDVEY 188

RESULT 7

S02724 streptokinase A precursor - Streptococcus pyogenes (strain SF130/13)

C:Species: Streptococcus pyogenes

C:Date: 18-Oct-1989 #sequence\_revision 18-Oct-1989 #text\_change 22-Jun-1999

C:Accession: S02724

R:Walter, F.; Siegel, M.; Maize, H.

Nucleic Acids Res. 17, 1261, 1989

A:Title: Nucleotide sequence of the streptokinase gene from a Streptococcus pyogenes type

A:Reference number: S02724; MUID:89160264; PMID:2646590

A:Accession: S02724

A:Molecule type: DNA

A:Residues: 1-440 <MAL>

A:Cross-references: EMBL:X13399; NID:G47435; PIDN:CAA31765.1; PID:G47436

C:Genetics:

A:Gene: ska

C:Superfamily: streptokinase

F:1-26/Domain: signal sequence #status predicted <SIG>

F:27-440/Product: streptokinase #status predicted <MAT>

Query Match 100.0%; Score 30; DB 2; Length 440;

Best Local Similarity 100.0%; Pred. No. 28;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVDVEY 6

|||||

Db 183 SVDVEY 188

RESULT 8

T10729

transferrin-like protein Ttf-1, salt-induced - green alga (Dunaliella salina)

C:Species: Dunaliella salina

C:Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 16-Jul-1999

C:Accession: T10729

R:Fisher, M.; Gokhman, I.; Pick, U.; Zamir, A.

submitted to the EMBL Data Library, November 1996

A:Reference number: Z17101

A:Accession: T10729

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-1274 <FIS>

A:Cross-references: EMBL:U77059; NID:G1684791; PID:G1684792

C:Genetics:

A:Gene: ttf1

C:Superfamily: transferrin repeat homology

Query Match 100.0%; Score 30; DB 2; Length 1274;

Best Local Similarity 100.0%; Pred. No. 90;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVDVEY 6

|||||

Db 1186 SVDVEY 1191

RESULT 9

T31951

hypothetical protein B0047.4 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 29-Oct-1999

C:Accession: T31951

R:Pauley, A.; Goela, D.; Ozersky, P.

submitted to the EMBL Data Library, July 1997

A:Description: The sequence of C. elegans cosmid B0047.

A:Reference number: Z21102

A:Accession: T31951

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-186 <PAU>

A:Cross-references: EMBL:AF016658; PIDN:AAB66044.1; GSPDB:GN00020; CESP:B0047.4

A:Experimental source: strain Bristol N2; clone B0047

C:Genetics:

A:Gene: CESP:B0047.4

A:Map position: 2

A:Introns: 51/2

Query Match 96.7%; Score 29; DB 2; Length 186;

Best Local Similarity 83.3%; Pred. No. 19;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVDVEY 6

|||||

Db 79 SVDVEY 84

RESULT 10

C97297

probable phosphatase, HAD superfamily [imported] - Clostridium acetobutylicum

C:Species: Clostridium acetobutylicum

C:Date: 14-Sep-2001 #sequence\_revision 14-Sep-2001 #text\_change 14-Sep-2001

C:Accession: C97297

R:Nolling, J.; Bretton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Lee

J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.

J. Bacteriol. 183, 4823-4838, 2001

A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Cl

A:Reference number: A96900; MUID:21359325; PMID:21359325

A:Accession: C97297

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-215 <KUR>

A:Cross-references: GB:AE001437; PIDN:AAK81166.1; PID:G15026304; GSPDB:GN00168

A:Experimental source: Clostridium acetobutylicum ATCC824

C:Genetics:

A:Gene: CAC3231

Query Match 96.7%; Score 29; DB 2; Length 215;

Best Local Similarity 83.3%; Pred. No. 22;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVDVEY 6

|||||

Db 25 SVDVEY 30

RESULT 11

T16011

hypothetical protein F09F7.3 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 24-Nov-1999

C:Accession: T16011

R:Pauley, A.

submitted to the EMBL Data Library, May 1994

A:Description: The sequence of C. elegans cosmid F09F7.

A:Reference number: Z18445

A:Accession: T16011

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-1207 <PAU>

A:Cross-references: EMBL:U00050; NID:G4851108; PID:G4851110; PIDN:AAA50695.1; CESP:F09F7.3

A:Experimental source: strain Bristol N2  
C:Genetics:  
A:Gene: CESP:F09F7.3  
A:Introns: 23/1; 297/3; 600/2; 630/2; 724/3; 789/3; 916/1; 1102/2; 1150/3  
C:Superfamily: DNA-directed RNA polymerase 132k polypeptide

Query Match 96.7%; Score 29; DB 2; Length 1207;  
Best Local Similarity 83.3%; Pred. No. 1.5e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVEY 6  
DB 170 SVDIEY 175

RESULT 12  
T31082  
endo-1,4-beta-xylanase (EC 3.2.1.8) - Caldicellulosiraptor sp.  
C:Species: Caldicellulosiraptor sp.  
C:Date: 02-Sep-2000 #sequence\_revision 02-Sep-2000 #text\_change 02-Sep-2000  
C:Accession: T31082  
R:Morris, D.D.; Gibbs, M.D.; Ford, M.; Thomas, J.; Bergquist, P.L.  
Submitted to the EMBL Data Library, December 1997  
A:Description: Family 10 and 11 xylanase genes from Caldicellulosiraptor sp. Rt698.1.  
A:Reference number: Z20972  
A:Accession: T31082  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-1595 <MOR>  
A:Cross-references: EMBL:AF036923; NID:g2760904; PID:g2760908; PIDN:AAB95325.1  
C:Genetics:  
A:Gene: xynB  
C:Keywords: glycosidase; hydrolase

Query Match 96.7%; Score 29; DB 2; Length 1595;  
Best Local Similarity 83.3%; Pred. No. 2e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVEY 6  
DB 1548 SVDIEY 1553

RESULT 13  
IQBS44  
primosome component (helicase loader) dnaI - Bacillus subtilis  
N:Alternate names: dnaA protein homolog, 44K, hypothetical protein Y (dnaB 3' region)  
C:Species: Bacillus subtilis  
C:Date: 31-Mar-1993 #sequence\_revision 31-Mar-1993 #text\_change 19-Jan-2001  
C:Accession: B24720; C26580; F69617  
R:Ogasawara, N.; Moriya, S.; Mazza, P.G.; Yoshikawa, H.  
Nucleic Acids Res. 14, 9989-9999, 1986  
A:Title: Nucleotide sequence and organization of dnaB gene and neighbouring genes on the  
A:Reference number: A93650; MUID:87117549; PMID:3027671  
A:Accession: B24720  
A:Molecule type: DNA  
A:Residues: 1-311 <OGA>  
A:Cross-references: GB:X04963; NID:g39880; PIDN:CAA28633.1; PID:g39881  
R:Hoshino, T.; McKenzie, T.; Schmidt, S.; Tanaka, T.; Sueoka, N.  
Proc. Natl. Acad. Sci. U.S.A. 84, 653-657, 1987  
A:Title: Nucleotide sequence of Bacillus subtilis dnaB: a gene essential for DNA replica  
A:Reference number: A94709; MUID:87118226; PMID:3027697  
A:Accession: C26580  
A:Molecule type: DNA  
A:Residues: 1-18, 'N', '20-23, 'T', '25-206 <EOS>  
R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter  
C.: Ehrlrich, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chd  
A.: Ehrlich, S.D.; Emmerison, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.  
Nature 390, 249-256, 1997  
A:Authors: Foulger, D.; Fritz, C.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galle  
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hulio, M.F.  
Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,  
A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel

Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelli  
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,  
A:Authors: Schleich, S.; Schroeter, R.; Scoffone, P.; Sekiguchi, J.; Sekowska, A.; Seroi  
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,  
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yaumoto, K.; Yata, K.; Yoshida, I  
A:Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Dachin, A.  
A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.  
A:Reference number: A69580; MUID:98044033; PMID:9384377  
A:Accession: F69617  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-311 <KUN>  
A:Cross-references: GB:Z39118; GB:AL009126; NID:g2635200; PIDN:CAB14858.1; PID:g2635363  
A:Experimental source: strain 168  
C:Genetics:  
A:Gene: dnaI  
C:Superfamily: 44K dnaA protein homolog  
C:Keywords: ATP; nucleotide binding; P-loop  
F:168-175/Region: nucleotide-binding motif A (P-loop)

Query Match 93.3%; Score 28; DB 1; Length 311;  
Best Local Similarity 66.7%; Pred. No. 58;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVEY 6  
DB 93 SVDIEY 98

RESULT 14  
T27619  
hypothetical protein ZC504.2 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 18-Feb-2000  
C:Accession: T27619  
R:Kershaw, J.  
Submitted to the EMBL Data Library, July 1995  
A:Reference number: Z20394  
A:Accession: T27619  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-629 <WIL>  
A:Cross-references: EMBL:Z50029; PIDN:CAA90341.1; GSPDB:GN00028; CESP:ZC504.2  
A:Experimental source: clone ZC504  
C:Genetics:  
A:Gene: CESP:ZC504.2  
A:Map position: X  
A:Introns: 11/3; 63/1; 114/3; 166/2; 187/3; 233/3; 348/2; 405/1; 431/2; 473/1; 581/3  
C:Superfamily: acetylcholine receptor

Query Match 93.3%; Score 28; DB 2; Length 629;  
Best Local Similarity 66.7%; Pred. No. 1.3e+02;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVEY 6  
DB 200 SVDIEY 205

RESULT 15  
A60745  
major outer membrane protein - Fusobacterium nucleatum (strain FeV1) (fragment)  
C:Species: Fusobacterium nucleatum  
C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 07-May-1999  
C:Accession: A60745  
R:Bakken, V.; Aaro, S.; Jensen, H.B.  
J. Gen. Microbiol. 135, 3253-3262, 1989  
A:Title: Purification and partial characterization of a major outer-membrane protein of  
A:Reference number: A60745; MUID:90257576; PMID:2636259  
A:Accession: A60745  
A:Molecule type: protein  
A:Residues: 1-50 <BAK>  
A:Note: sequences of the homologous protein from strains F6, F3, and ATCC 10953 were del



C;Keywords: membrane protein

Query Match 90.0%; Score 27; DB 2; Length 50;  
Best Local Similarity 83.3%; Pred. No. 13;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVDVEY 6  
|:|:|:|  
Db 38 SVDVQY 43

RESULT 16

C88465  
protein B0244.9 [imported] - Caenorhabditis elegans  
C;Species: Caenorhabditis elegans  
C;Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 10-May-2001  
C;Accession: C88465  
R;Anonymous, The C. elegans Sequencing Consortium.  
Science 283, 2012-2018, 1998  
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biology  
A;Reference number: A75000; MUID:99069613; PMID:9851916  
A;Note: see websites genome.wustl.edu/gsc/C\_elegans/ and www.sanger.ac.uk/Projects/C\_ele  
A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and  
A;Accession: C88465  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-180 <STO>  
A;Cross-references: GB:Chr\_III; PIDN:AAA68377.1; PID:g861357; GSPDB:GN00021; CESP:B0244.  
C;Genetics:  
A;Gene: B0244.9  
A;Map position: 3

Query Match 90.0%; Score 27; DB 2; Length 180;  
Best Local Similarity 83.3%; Pred. No. 55;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVDVEY 6  
|:|:|:|  
Db 8 SVDLEY 13

RESULT 17

G90898  
probable tail fiber protein [imported] - Escherichia coli (strain O157:H7, substrain RIM  
C;Species: Escherichia coli  
C;Date: 18-Jul-2001 #sequence\_revision 18-Jul-2001 #text\_change 18-Jul-2001  
C;Accession: G90898  
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.  
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.  
DNA Res. 8, 11-22, 2001  
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gene  
A;Reference number: A99629; MUID:21156231; PMID:11258796  
A;Accession: G90898  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-271 <HAY>  
A;Cross-references: GB:BA000007; PIDN:BA835582.1; PID:g13361625; GSPDB:GN00154  
A;Experimental source: strain O157:H7, substrain RIMD 050952  
C;Genetics:  
A;Gene: EC82159

Query Match 90.0%; Score 27; DB 2; Length 271;  
Best Local Similarity 83.3%; Pred. No. 86;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVDVEY 6  
|:|:|:|  
Db 52 SMDVEY 57

RESULT 18

B85842  
hypothetical protein Z3309 [imported] - Escherichia coli (strain O157:H7, substrain EDL9

C;Species: Escherichia coli  
C;Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 14-Sep-2001  
C;Accession: B85842  
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew  
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca  
Nature 409, 529-533, 2001  
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.  
A;Reference number: A85480; MUID:21074935; PMID:11206551  
A;Accession: B85842  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-271 <STO>  
A;Cross-references: GB:AE005174; NID:g12516359; PIDN:AAG57198.1; GSPDB:GN00145; UMG:P.23  
A;Experimental source: strain O157:H7, substrain EDL933  
C;Genetics:  
A;Gene: Z3309

Query Match 90.0%; Score 27; DB 2; Length 271;  
Best Local Similarity 83.3%; Pred. No. 86;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVDVEY 6  
|:|:|:|  
Db 52 SMDVEY 57

RESULT 19

JN0848  
outer membrane 40K protein precursor - Fusobacterium nucleatum (strain Fev1)  
C;Species: Fusobacterium nucleatum  
C;Date: 10-Mar-1994 #sequence\_revision 10-Mar-1994 #text\_change 08-Oct-1999  
C;Accession: JN0848  
R;Bolstad, A.I.; Jensen, H.B.  
Gene 132, 107-112, 1993  
A;Title: Complete sequence of omp1, the structural gene encoding the 40-kDa outer membr  
A;Reference number: JN0848; MUID:94010332; PMID:8406032  
A;Accession: JN0848  
A;Molecule type: DNA  
A;Residues: 1-368 <BOL>  
A;Cross-references: EMBL:X66735; NID:9404159; PIDN:CAA47273.1; PID:g404160  
A;Experimental source: strain Fev1  
C;Comment: This protein is involved  
C;Keywords: membrane protein; porin  
F.1-20/Domain: signal sequence #status predicted <SIG>  
F.20-368/Product: outer membrane 40K protein #status predicted <MAT>

Query Match 90.0%; Score 27; DB 2; Length 368;  
Best Local Similarity 83.3%; Pred. No. 1.2e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVDVEY 6  
|:|:|:|  
Db 59 SVDVQY 64

RESULT 20

S46435  
porin precursor - Fusobacterium nucleatum  
C;Species: Fusobacterium nucleatum  
C;Date: 14-Jul-1995 #sequence\_revision 21-Jul-1995 #text\_change 17-Nov-2000  
C;Accession: S46435; S51507  
R;Bolstad, A.I.; Tomassen, J.; Jensen, H.B.  
Mol. Gen. Genet. 244, 104-110, 1994  
A;Title: Sequence variability of the 40-kDa outer membrane proteins of Fusobacterium nu  
A;Reference number: S46435; MUID:94316187; PMID:8041356  
A;Accession: S46435  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-368 <BOL>  
A;Cross-references: EMBL:X72582  
R;Bolstad, A.I.  
submitted to the EMBL Data Library, August 1994  
A;Reference number: S51507

A;Accession: S51507  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-156, 'K', 158-368 <BO>  
A;Cross-references: EMBL:X72582; NID:g530295; PIDN:CAA51172.1; PID:g530296

Query Match 90.0%; Score 27; DB 2; Length 368;  
Best Local Similarity 83.3%; Pred. No. 1.2e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVEY 6  
|:|||||  
Db 59 SVDVQY 64

RESULT 21  
S46436  
Porin fona precursor - Fusobacterium nucleatum (ATCC 10953)  
N;Alternate names: major outer membrane protein, 40K  
C;Species: Fusobacterium nucleatum  
A;Variety: ATCC 10953  
C;Date: 14-Jul-1995 #sequence\_revision 21-Jul-1995 #text\_change 08-Oct-1999  
C;Accession: S46436; S51508  
R;Bolstad, A.I.; Tomassen, J.; Jensen, H.B.  
Mol. Gen. Genet. 244, 104-110, 1994  
A;Title: Sequence variability of the 40-kDa outer membrane proteins of Fusobacterium nucleatum  
A;Reference number: S46435; MUID:94316187; PMID:8041356  
A;Accession: S46436  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-371 <BO>  
A;Cross-references: EMBL:X72583  
A;Experimental source: ATCC 10953  
R;Bolstad, A.I.  
submitted to the EMBL Data Library, March 1993  
A;Reference number: S51508  
A;Accession: S51508  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-38 'E', 40-338 'G', 340-363 'S', 365-371 <BO>  
A;Cross-references: EMBL:X72583; NID:g551439; PIDN:CAA51173.1; PID:g551440  
A;Experimental source: ATCC 10953  
C;Genetics:  
A;Gene: fona  
C;Keywords: transmembrane protein  
F;1-20/Domain: signal sequence #status predicted <SIG>  
F;21-371/Product: porin #status predicted <VAR>

Query Match 90.0%; Score 27; DB 2; Length 371;  
Best Local Similarity 83.3%; Pred. No. 1.2e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVEY 6  
|:|||||  
Db 59 SVDVQY 64

RESULT 22  
G85631  
hypothetical protein Z1382 [imported] - Escherichia coli (strain O157:H7, substrain EDL933)  
C;Species: Escherichia coli  
C;Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 03-Jun-2002  
C;Accession: G85631  
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew  
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamianos, K.; Apodaca,  
Nature 409, 529-533, 2001  
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.  
A;Reference number: A85480; MUID:21074935; PMID:11206551  
A;Accession: G85631  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-375 <STO>  
A;Cross-references: GB:AE005174; NID:g12514226; PIDN:AAG55515.1; GSPDB:GN00145; UWGP:Z13

A;Experimental source: strain O157:H7, substrain EDL933  
C;Genetics:  
A;Gene: Z1382  
C;Superfamily: phage lambda hypothetical protein 401

Query Match 90.0%; Score 27; DB 2; Length 375;  
Best Local Similarity 83.3%; Pred. No. 1.2e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVEY 6  
|:|||||  
Db 52 SMDVEY 57

RESULT 23  
S61704  
probable transcription factor YPL230W - yeast (Saccharomyces cerevisiae)  
N;Alternate names: hypothetical protein Pl421  
C;Species: Saccharomyces cerevisiae  
C;Date: 09-Mar-1996 #sequence\_revision 12-Apr-1996 #text\_change 19-Apr-2002  
C;Accession: S61704; S65249; S65255  
R;Urrestarazu, L.A.  
submitted to the EMBL Data Library, December 1995  
A;Reference number: S61699  
A;Accession: S61704  
A;Molecule type: DNA  
A;Residues: 1-391 <UR>  
A;Cross-references: EMBL:X94561; NID:g1181252; PID:e217970; PID:g1181258  
R;Rieger, M.; Mueller-Auer, S.; Schaefer, M.  
submitted to the Protein Sequence Database, May 1996  
A;Reference number: S65202  
A;Accession: S65249  
A;Molecule type: DNA  
A;Residues: 1-391 <RI>  
A;Cross-references: EMBL:Z73586; NID:g1370475; PID:e246942; PID:g1370476; MIPS:YPL230W  
A;Experimental source: strain S288C (AB972)  
R;Urrestarazu, L.A.; Visse, S.  
submitted to the Protein Sequence Database, May 1996  
A;Reference number: S65251  
A;Accession: S65255  
A;Molecule type: DNA  
A;Residues: 1-391 <UR>  
A;Cross-references: EMBL:Z73586; NID:g1370475; PID:e246942; PID:g1370476; MIPS:YPL230W  
A;Experimental source: strain S288C (AB972)  
C;Genetics:  
A;Gene: SGD:USV1  
A;Cross-references: SGD:S0006151  
A;Map position: 16L

Query Match 90.0%; Score 27; DB 2; Length 391;  
Best Local Similarity 83.3%; Pred. No. 1.3e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVEY 6  
|:|||||  
Db 228 SVDVQY 233

RESULT 24  
E70598  
probable PPE protein - Mycobacterium tuberculosis (strain H37RV)  
C;Species: Mycobacterium tuberculosis  
C;Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 22-Oct-1999  
C;Accession: E70598  
R;Cole, S.T.; Broesch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Hartis, D.; Gordon,  
Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.  
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.  
Nature 393, 537-544, 1998  
A;Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.  
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome  
A;Reference number: A70500; MUID:98295987; PMID:9634230  
A;Accession: E70598  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA  
A:Residues: 1-399 <COL>  
A:Cross-references: GB:Z94121; GB:AL123456; NID:g3261736; PIDN:CAB08082.1; PID:e312285;  
A:Experimental source: strain H37RV  
C:Genetics:  
A:Gene: PPE

Query Match 90.0%; Score 27; DB 2; Length 399;  
Best Local Similarity 83.3%; Pred. No. 1.3e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVEY 6  
|:||||  
Db 139 SLDVEY 144

RESULT 25  
QXB21L  
Hypothetical protein 401 - phage lambda  
N:Alternate names: orf-401; orf401  
C:Species: Phage lambda  
C:Date: 13-Jun-1993 #sequence\_revision 13-Jun-1983 #text\_change 23-Jul-1999  
C:Accession: G43010; D43016; A04389  
R:Daniels, D. submitted to the Nucleic Acid Sequence Database, September 1982  
A:Reference number: A94614  
A:Accession: G43010  
A:Molecule type: DNA  
A:Residues: 1-401 <DAN>  
R:Sanger, F.; Coulson, A.R.; Hong, G.F.; Hill, D.F.; Petersen, G.B.  
J. Mol. Biol. 162, 729-773, 1982  
A:Title: Nucleotide sequence of bacteriophage lambda DNA.  
A:Reference number: A92891; MUID:83189071; PMID:6221115  
A:Accession: D43016  
A:Molecule type: DNA  
A:Residues: 1-401 <SAN>  
A:Cross-references: GB:J02459; GB:M17233; GB:M24325; GB:V00636; GB:X00906; NID:g215104;  
C:Genetics:  
A:Map position: 40.51-42.99  
C:Superfamily: phage lambda hypothetical protein 401

Query Match 90.0%; Score 27; DB 1; Length 401;  
Best Local Similarity 83.3%; Pred. No. 1.3e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVEY 6  
|:||||  
Db 50 SMDVEY 55

RESULT 26  
G90907  
Probable tail fiber protein [imported] - Escherichia coli (strain O157:H7, substrain R11)  
C:Species: Escherichia coli  
C:Date: 18-Jul-2001 #sequence\_revision 18-Jul-2001 #text\_change 17-May-2002  
C:Accession: G90907  
R:Havashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.  
R:Hayashi, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.  
DNA Res. 8, 11-22, 2001  
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gen  
A:Reference number: A99629; MUID:21156231; PMID:11258796  
A:Accession: G90907  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-407 <HAY>  
A:Cross-references: GB:BA000007; PIDN:BAB35654.1; PID:gl3361697; GSPDB:GN00154  
A:Experimental source: strain O157:H7, substrain R1MD 0509952  
C:Genetics:  
A:Gene: ECs2231  
C:Superfamily: phage lambda hypothetical protein 401

Query Match 90.0%; Score 27; DB 2; Length 407;  
Best Local Similarity 83.3%; Pred. No. 1.4e+02;

```

R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gen
A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: F50854
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-437 <HAY>
A;Cross-references: GB:BA000007; PIDN:BA035231.1; PID:gl3361273; GSPDB:GN00154
A;Experimental source: strain O157:H7, substrain RIMD 0509952
C;Genetics:
A;Gene: ECs1808
C;Superfamily: phage lambda hypothetical protein 401

Query Match          90.0%; Score 27; DB 2; Length 437;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 SVDVEY 6
       |:|||||
Db      50 SMDVEY 55

RESULT 30
D90734
Probable tail fiber protein [imported] - Escherichia coli (strain O157:H7, substrain RIM
C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Jun-2002
C;Accession: D90734
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gen
A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: D90734
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-438 <HAY>
A;Cross-references: GB:BA000007; PIDN:BA034267.1; PID:gl3360303; GSPDB:GN00154
A;Experimental source: strain O157:H7, substrain RIMD 0509952
C;Genetics:
A;Gene: ECs0844
C;Superfamily: phage lambda hypothetical protein 401

Query Match          90.0%; Score 27; DB 2; Length 438;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 SVDVEY 6
       |:|||||
Db      51 SMDVEY 56

RESULT 31
C90769
Probable tail fiber protein [imported] - Escherichia coli (strain O157:H7, substrain RIM
C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 17-May-2002
C;Accession: C90769
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gen
A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: C90769
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-439 <HAY>
A;Cross-references: GB:BA000007; PIDN:BA034546.1; PID:gl3360583; GSPDB:GN00154
A;Experimental source: strain O157:H7, substrain RIMD 0509952
C;Genetics:
A;Gene: ECs1123

C;Superfamily: phage lambda hypothetical protein 401
Query Match          90.0%; Score 27; DB 2; Length 439;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 SVDVEY 6
       |:|||||
Db      52 SMDVEY 57

RESULT 32
B85816
Probable tail fiber protein of prophage CP-9330 Z3074 [imported] - Escherichia coli (st
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 17-May-2002
C;Accession: B85816
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhe
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamouisis, K.; Apodaca
Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: B85816
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-439 <STO>
A;Cross-references: GB:AS005174; NID:gl2516091; PIDN:AAG56993.1; GSPDB:GN00145; UWGP:Z3
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
A;Gene: Z3074
C;Superfamily: phage lambda hypothetical protein 401

Query Match          90.0%; Score 27; DB 2; Length 439;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 SVDVEY 6
       |:|||||
Db      52 SMDVEY 57

RESULT 33
A85719
Probable tail fiber protein of prophage CP-9330 Z2147 [imported] - Escherichia coli (st
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 03-Jun-2002
C;Accession: A85719
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhe
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamouisis, K.; Apodaca
Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: A85719
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-439 <STO>
A;Cross-references: GB:AS005174; NID:gl2515104; PIDN:AAG56213.1; GSPDB:GN00145; UWGP:Z2
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
A;Gene: Z2147
C;Superfamily: phage lambda hypothetical protein 401

Query Match          90.0%; Score 27; DB 2; Length 439;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 SVDVEY 6
       |:|||||
Db      52 SMDVEY 57

RESULT 34
A85741

```

hypothetical protein Z2340 [imported] - Escherichia coli (strain O157:H7, substrain EDL958)  
C:Species: Escherichia coli  
C>Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 03-Jun-2002  
C:Accession: A85741  
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew  
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,  
Nature 409, 529-533, 2001  
A>Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.  
A:Reference number: A85480; MUID:21074935; PMID:11206551  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-439 <STO>  
A:Cross-references: GB:AE005174; NID:gl2515332; PIDN:AAG56389.1; GSPDB:GN00145; UWGP:Z23  
A:Experimental source: strain O157:H7, substrain EDL933  
C:Genetics:  
A:Gene: Z2340  
C:Superfamily: phage lambda hypothetical protein 401

Query Match 90.0%; Score 27; DB 2; Length 439;  
Best Local Similarity 83.3%; Pred. No. 1.5e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVEY 6  
|:|||||  
Db 52 SMDVEY 57

RESULT 35  
F85584  
Probable tail component of prophage CP-933K Z0982 [imported] - Escherichia coli (strain  
C:Species: Escherichia coli  
C>Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 03-Jun-2002  
C:Accession: F85584  
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew  
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,  
Nature 409, 529-533, 2001  
A>Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.  
A:Reference number: A85480; MUID:21074935; PMID:11206551  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-440 <STO>  
A:Cross-references: GB:AE005174; NID:gl2513753; PIDN:AAG55138.1; GSPDB:GN00145; UWGP:Z09  
A:Experimental source: strain O157:H7, substrain EDL933  
C:Genetics:  
A:Gene: Z0982  
C:Superfamily: phage lambda hypothetical protein 401

Query Match 90.0%; Score 27; DB 2; Length 440;  
Best Local Similarity 83.3%; Pred. No. 1.5e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVEY 6  
|:|||||  
Db 53 SMDVEY 58

RESULT 36  
H81971  
Probable ABC transporter ATP-binding protein NMA0535 [imported] - Neisseria meningitidis  
C:Species: Neisseria meningitidis  
C>Date: 05-May-2000 #sequence\_revision 05-May-2000 #text\_change 02-Feb-2001  
C:Accession: H81971  
R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel  
; Holroyd, S.; Jagers, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,  
Nature 404, 502-506, 2000  
A>Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.  
A:Reference number: A81775; MUID:20222556; PMID:10761919  
A:Accession: H81971  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-621 <PAR>

A:Cross-references: GB:AL162753; GB:AL157959; NID:g7379120; PIDN:CAB83829.1; PID:g73792  
A:Experimental source: serogroup A, strain Z2491  
C:Genetics:  
A:Gene: NMA0535  
C:Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homology

Query Match 90.0%; Score 27; DB 2; Length 621;  
Best Local Similarity 83.3%; Pred. No. 2.2e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVEY 6  
|:|||||  
Db 380 NVDVEY 385

RESULT 37  
C81026  
ABC transporter, ATP-binding protein NMB1919 [imported] - Neisseria meningitidis (strain  
C:Species: Neisseria meningitidis  
C>Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 19-Jan-2001  
C:Accession: C81026  
R:Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.  
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.  
ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Maignani, V.; Pizza, M.  
Science 287, 1809-1815, 2000  
A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; V  
A>Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.  
A:Reference number: A81000; MUID:20175755; PMID:10710307  
A:Accession: C81026  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-621 <TET>  
A:Cross-references: GB:AE002541; GB:AE002098; NID:g7227175; PIDN:AAF42249.1; PID:g72271  
A:Experimental source: serogroup B, strain MC58  
C:Genetics:  
A:Gene: NMB1919  
C:Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homology

Query Match 90.0%; Score 27; DB 2; Length 621;  
Best Local Similarity 83.3%; Pred. No. 2.2e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVEY 6  
|:|||||  
Db 380 NVDVEY 385

RESULT 38  
E96830  
hypothetical protein F18B13.1 [imported] - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C>Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 23-Mar-2001  
C:Accession: E96830  
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso  
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.  
ansen, N.F.; Hughes, B.; Huizar, L.  
Nature 408, 816-820, 2000  
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C  
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali  
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,  
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
A>Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
A:Reference number: A86141; MUID:21016719; PMID:11130712  
A:Accession: E96830  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-831 <STO>  
A:Cross-references: GB:AE005173; NID:g5902359; PIDN:AAD55461.1; GSPDB:GN00141  
C:Genetics:  
A:Gene: F18B13.1  
A:Map position: 1  
C:Superfamily: heat shock protein 91

Query Match 90.0%; Score 27; DB 2; Length 831;  
 Best Local Similarity 83.3%; Pred. No. 3.e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVEY 6  
 |||||  
 Db 445 SVDVQY 450

RESULT 39  
 JC4624  
 A:Title: Molecular cloning, sequencing, and expression of a cDNA encoding alpha-glucosidase from *Rhizomucor circinelloides* f. *circinelloides*  
 C:Species: *Rhizomucor circinelloides* f. *circinelloides*  
 C>Date: 10-May-1996 #sequence\_revision 19-Jul-1996 #text\_change 20-Jun-2000  
 C:Accession: J04624; PC4149  
 R: Sugimoto, M.; Suzuki, Y.  
 J. Biochem. 119, 500-505, 1996  
 A:Reference number: J04624; MUID:96271012; PMID:8830045  
 A:Accession: J04624  
 A:Molecule type: mRNA  
 A:Residues: 1-864 <SUG1>  
 A:Cross-references: DBJ:D67034; NID:G1498134; PIDN:BAA11053.1; PID:G1498135  
 A:Accession: PC4149  
 A:Molecule type: protein  
 A:Residues: 203-214; 492-495; 612-623; 715-731; 742-751; 769-778 <SUG2>  
 A:Note: the source is designated as *Mucor javanicus* IFO4570  
 C:Comment: This enzyme is an exo-carbohydrase, and catalyzes the splitting of an alpha-1,4-glycosidic bond in soluble starch.  
 C:Superfamily: lysosomal alpha-glucosidase; sucrose/isomaltase homology; trefoil homolog  
 C:Keywords: glycoprotein; glycosidase; hydrolase  
 F:122-805/Domain: sucrose/isomaltase homology <SIM>  
 F:187,364,406,466,500,568,734/Binding site: carbohydrate (Asn) (covalent) #status predicted  
 F:430/Active site: Asp #status predicted

Query Match 90.0%; Score 27; DB 2; Length 864;  
 Best Local Similarity 83.3%; Pred. No. 3.1e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVEY 6  
 |||||  
 Db 75 TVDVEY 80

RESULT 40  
 B90835  
 A:Title: Probable tail fiber protein [imported] - *Escherichia coli* (strain O157:H7, substrain RIM)  
 C:Species: *Escherichia coli*  
 C>Date: 18-Jul-2001 #sequence\_revision 18-Jul-2001 #text\_change 18-Jul-2001  
 C:Accession: B90835  
 R: Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.O.; Sasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.  
 DNA Res. 8, 11-22, 2001  
 A:Title: Complete genome sequence of enterohemorrhagic *Escherichia coli* O157:H7 and genome analysis  
 A:Reference number: A99629; MUID:21156231; PMID:11258796  
 A:Accession: B90835  
 A>Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-971 <HAY>  
 A:Cross-references: GB:BA000007; PIDN:BA035073.1; PID:G13361114; GSPDB:GN00154  
 A:Experimental source: strain O157:H7, substrain RIMD 0509952  
 C:Genetics:  
 A:Gene: ECs1650

Query Match 90.0%; Score 27; DB 2; Length 971;  
 Best Local Similarity 83.3%; Pred. No. 3.6e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVEY 6  
 |||||  
 Db 50 SMDVEY 55

RESULT 41  
 C85693  
 A:Title: Probable membrane protein of prophage CP-933X Z1918 [imported] - *Escherichia coli* (extra)  
 C:Species: *Escherichia coli*  
 C>Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 14-Sep-2001  
 C:Accession: C85693  
 R: Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamocuous, K.; Apodaca, Nature 409, 529-533, 2001  
 A:Title: Genome sequence of enterohemorrhagic *Escherichia coli* O157:H7.  
 A:Reference number: A85480; MUID:21074935; PMID:11206551  
 A:Accession: C85693  
 A>Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-973 <STO>  
 A:Cross-references: GB:AE005174; NID:G12514847; PIDN:AA056007.1; GSPDB:GN00145; UNGP:Z1  
 A:Experimental source: strain O157:H7, substrain EDU933  
 C:Genetics:  
 A:Gene: Z1918

Query Match 90.0%; Score 27; DB 2; Length 973;  
 Best Local Similarity 83.3%; Pred. No. 3.6e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVEY 6  
 |||||  
 Db 52 SMDVEY 57

RESULT 42  
 D90387  
 A:Title: Peptidase related protein [imported] - *Sulfolobus solfataricus*  
 C:Species: *Sulfolobus solfataricus*  
 C>Date: 24-May-2001 #sequence\_revision 24-May-2001 #text\_change 24-May-2001  
 C:Accession: D90387  
 R: She, O.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan, J.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, arrett, R.A.; Regan, M.A.; Sensen, C.W.; Van der Coest, J.  
 Submitted to GenBank, April 2001  
 A:Description: *Sulfolobus solfataricus* complete genome.  
 A:Reference number: A99139  
 A:Accession: D90387  
 A>Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-1077 <KUR>  
 A:Cross-references: GB:AE006641; NID:G13815479; PIDN:AAK42355.1; GSPDB:GN00155  
 C:Genetics:  
 A:Gene: SSO2181

Query Match 90.0%; Score 27; DB 2; Length 1077;  
 Best Local Similarity 83.3%; Pred. No. 4e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVEY 6  
 |||||  
 Db 246 SLDVEY 251

RESULT 43  
 G64887  
 A:Title: Probable tail fiber protein GP37 - *Escherichia coli* (strain K-12)  
 C:Species: *Escherichia coli*  
 C>Date: 12-Sep-1997 #sequence\_revision 17-Sep-1997 #text\_change 01-Mar-2002  
 C:Accession: G64887; TC9189  
 R: Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Science 277, 1453-1462, 1997  
 A:Title: The complete genome sequence of *Escherichia coli* K-12.  
 A:Reference number: A64720; MUID:97426617; PMID:9278503  
 A:Accession: G64887  
 A>Status: nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA

A;Residues: 1-1122 <BLAT>  
A;Cross-references: GB:AE000234; GB:U00096; NID:g1787633; PIDN:AACT74454.1; PID:g1787636;  
A;Experimental source: strain K-12, substrain MG1655  
R;Alba, H.; Baba, T.; Fujita, K.; Hayashi, K.; Inada, T.; Isono, K.; Itoh, T.; Kaaai, H.  
; Motomura, K.; Nakade, S.; Nakamura, Y.; Naehimoto, H.; Nishio, Y.; Oshima, T.; Saico,  
moto, Y.; Horiuchi, T.  
DNA Res. 3, 363-377, 1996  
A;Title: A 570-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the  
A;Reference number: Z16603; MUID:97251357; PMID:9097039  
A;Accession: T09189  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 3-1122 <AIB>  
A;Cross-references: GB:AE000234; GB:U00096; NID:g1787633; PIDN:AACT74454.1; PID:g1787636;  
Query Match 90.0%; Score 27; DB 2; Length 1122;  
Best Local Similarity 83.3%; Pred. No. 4.2e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SVDVEY 6  
|:|||||  
Db 52 SMDVEY 57

RESULT 44  
S30790  
Myosin MYO4 - Yeast (Saccharomyces cerevisiae)  
N;Alternate names: protein YAL029c  
N;Contains: myosin ATPase (EC 3.6.4.1)  
C;Species: Saccharomyces cerevisiae  
C;Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 19-Apr-2002  
A;Accession: S30790; S51991  
R;Haarer, B.K.; Brown, S.S.  
submitted to the EMBL Data Library, March 1992  
A;Description: Identification of a yeast myosin gene that is similar to the yeast MYO2 g  
A;Reference number: S30790  
A;Accession: S30790  
A;Molecule type: DNA  
A;Residues: 1-1471 <HAA>  
A;Cross-references: EMBL:M90057; NID:g172023; PIDN:AACT37409.1; PID:g172024  
R;Bussey, H.; Kaback, D.B.; Zhong, W.; Vo, D.T.; Clark, M.W.; Fortin, N.; Hall, J.; Ouel  
submitted to the EMBL Data Library, August 1994  
A;Description: The sequence of chromosome 1 of Saccharomyces cerevisiae.  
A;Reference number: S51956  
A;Accession: S51991  
A;Molecule type: DNA  
A;Residues: 1-1471 <BUS>  
A;Cross-references: EMBL:U12980; NID:g1326053; PIDN:AACT05003.1; PID:G595556; GSPDB:GN000  
C;Comment: The neck domain comprises six approximately 23-residue tandem repeats; this d  
C;Genetics:  
A;Gene: SGD:MYO4; SHEL: FUN22; MIPS:YAL029c  
A;Cross-references: SGD:S0000027; MIPS:YAL029c  
A;Map position: 1L  
C;Superfamily: myosin MYO2; myosin motor domain homology  
C;Keywords: actin binding; ATP; coiled coil; hydrolase; nucleotide binding; P-loop; tand  
F;74-765/Domain: myosin motor domain homology <MYOT>  
F;165-172/Region: nucleotide-binding motif A (P-loop)  
F;648-669/Region: actin binding #status predicted  
F;778-922/Domain: neck #status predicted <NEC>  
F;938-1063/Domain: coiled coil #status predicted <COI>  
F;1064-1471/Domain: carboxyl-terminal #status predicted <CTD>  
F;171/Binding site: ATP (Lys) #status predicted  
F;688,698/Active site: Cys #status predicted

Query Match 90.0%; Score 27; DB 1; Length 1471;  
Best Local Similarity 83.3%; Pred. No. 5.7e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SVDVEY 6  
|:|||||  
Db 568 AVDVEY 573

RESULT 45  
JQ1899  
genome polyprotein - papaya ringspot virus  
N;Contains: 46K protein; 63K protein; 6K protein; coat protein; cylindrical inclusion p  
C;Species: papaya ringspot virus, PRSV  
C;Date: 30-Sep-1993 #sequence\_revision 20-Aug-1994 #text\_change 02-Feb-2001  
A;Accession: JQ1899; PQ0509; A56603; S24785; S35725  
R;Yeh, S.D.; Jan, F.J.; Chiang, C.H.; Doong, T.J.; Chen, M.C.; Chung, P.H.; Bau, H.J.  
J. Gen. Virol. 73, 2531-2541, 1992  
A;Title: Complete nucleotide sequence and genetic organization of papaya ringspot virus  
A;Reference number: JQ1899; MUID:93019006; PMID:1402799  
A;Accession: JQ1899  
A;Molecule type: genomic RNA  
A;Residues: 1-3344 <YEH1>  
A;Cross-references: GB:S46722; NID:g258106; PIDN:AAAB23789.1; PID:g258107  
A;Accession: PQ0509  
A;Molecule type: protein  
A;Residues: 548-554; 1402-1410 <YEH2>  
R;Wang, C.H.; Yeh, S.D.  
Arch. Virol. 127, 345-354, 1992  
A;Title: Nucleotide sequence comparison of the 3'-terminal regions of severe, mild, and  
A;Reference number: A56603; MUID:93090098; PMID:1456896  
A;Accession: A56603  
A;Molecule type: genomic RNA  
A;Residues: 2561-3344 <WAN>  
A;Cross-references: EMBL:X67672; NID:G62378; PIDN:CAA47904.1; PID:g62379  
A;Experimental source: type P, strain HA  
C;Superfamily: tobacco etch virus genome polyprotein  
C;Keywords: ATP; coat protein; cylindrical inclusion protein; genome-linked protein; in  
F;1-547/Protein: 63K protein #status predicted <PRO>  
F;548-1004/Product: helper component-proteinase #status predicted <HCP>  
F;11005-1401/Product: 46K protein #status predicted <PRT>  
F;1402-2036/Product: cylindrical inclusion protein #status predicted <CIP>  
F;1486-1493/Region: nucleotide-binding motif A (P-loop)  
F;1571-1576/Region: nucleotide-binding motif B  
F;1575-1578/Region: DEXH motif  
F;2037-2093/Product: 6K protein #status predicted <PRI>  
F;2094-2520/Product: nuclear inclusion a protein #status predicted <NIA>  
F;2521-3037/Product: nuclear inclusion b protein #status predicted <NIB>  
F;3038-3344/Product: coat protein #status predicted <COP>  
F;2156/Binding site: phosphoryl-RNA (Tyr) (covalent) #status predicted

Query Match 90.0%; Score 27; DB 2; Length 3344;  
Best Local Similarity 83.3%; Pred. No. 1.4e+03;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SVDVEY 6  
|:|||||  
Db 149 SVDLEY 154

RESULT 46  
F30945  
hypothetical protein ECs2534 [imported] - Escherichia coli (strain O157:H7, substrain R  
C;Species: Escherichia coli  
C;Date: 18-Jul-2001 #sequence\_revision 18-Jul-2001 #text\_change 18-Jul-2001  
A;Accession: F30945  
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G  
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.  
DNA Res. 8, 11-22, 2001  
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gen  
A;Reference number: A99629; MUID:21156231; PMID:11258796  
A;Accession: F30945  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-47 <HAY>  
A;Cross-references: GB:BA000007; PIDN:BAB35957.1; PID:g13362001; GSPDB:GN00154  
A;Experimental source: strain O157:H7, substrain RMD 050952  
C;Genetics:  
A;Gene: ECs2534

Query Match 86.7%; Score 26; DB 2; Length 47;  
Best Local Similarity 100.0%; Pred. No. 22;

```

Matches      5;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

Qy           2  VDVEY  6
              |||||
Db           14  VDVEY  18

RESULT  47
A85794
hypothetical protein Z2869 [imported] - Escherichia coli (strain O157:H7, substrain EDL93)
C:Species: Escherichia coli

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C/Accession: A85794  
C/Revision: 16-Feb-2001  
C/Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_Change 14-Sep-2001  
R/Perma, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew  
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamoudis, K.; Apodaca,  
R. K.; Karp, P.

Nature 409, 525-533, 2001  
A:Title: Genome sequence of enterohemorrhagic *Escherichia coli* O157:H7.  
A:Reference number: A85480; MUID:21074935; PMID:11206551  
A:Accession: A85794

```

A;Molecule type: DNA
A;Residues: 1-47 <STO>
A;Cross-references: GB:AE005174; NID:g12515870; PIDN:AAG56813.1; GSPDB:GN00145; UWGP:Z2869
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
A;Gene: Z2869

Query Match      86.7%   Score 26;   DB 2;   Length 47;
Best Local Similarity 100.0%;   Pred. No. 22;
Matches      5;   Conservative      0;   Mismatches      0;   Indels      0;   Gaps      0;

Qy      2   VDVEY 6
          |||||
Db      14   VDVEY 18

RESULT 48

```

H04943  
 hypothetical protein b1824 - *Escherichia coli* (strain K-12)  
 C:Species: *Escherichia coli*  
 C:Date: 12-Sep-1997 #sequence revision 17-Sep-1997 #text change 01-Mar-2002

C/Blattner: F8343  
R; Blattner, H.K.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cohen, D.A.; Rose, D.J.; Mau, B.; Shao, Y. Science 277, 1453-1462, 1997

A;Accession: H64943  
A;Reference number: A84720; MUID:9/426617; PMID:19278503  
A;Status: nucleic acid sequence not shown; translation not shown

Query Match	86.7%	Score 26;	DB 2;	Length 47;
Best Local Similarity	100.0%;	Pred. No. 22;		
Matches 5;	Conservative	0;	Mismatches	0;
Indels	0;	Gaps	0;	

Qy 2 VDVEX 6  
|||  
Db 14 VDVEX 18

RESULT 49  
AF0727  
conserved hypothetical protein STV1969 [imported] - Salmonella enterica subsp. enterica  
C/Species: Salmonella enterica subsp. enterica serovar Typhi  
A/Note: this species has also been called Salmonella typhi  
C/Date: 09-Nov-2001 #sequence\_revision 09-Nov-2001 #text\_change 18-Nov-2002  
C/Accession: AF0727  
R/Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,  
th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrah,  
S.; Moulé, S.; O'Gaora, P.



GenCore version 5.1.1.6  
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OM protein - protein search, using sw model

Run on: January 20, 2004, 13:54:52 ; Search time 11 Seconds  
(without alignments)  
25.651 Million cell updates/sec

Title: US-09-919-703-1

Perfect score: 30

Sequence: 1 SVDVY 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 75 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	30	100.0	280	1	LEC2_MEDTR
2	30	100.0	440	1	STRP_STREQ
3	30	100.0	440	1	STRP_STRPY
4	30	100.0	440	1	STRP_STRSP
5	29	96.7	183	1	Y34A_METJA
6	29	96.7	360	1	DCUP_WIGER
7	29	96.7	742	1	COG7_DROME
8	28	93.3	311	1	DNAI_BACSU
9	27	90.0	562	1	TPPI_MOUSE
10	27	90.0	563	1	TPPI_CANFA
11	27	90.0	563	1	TPPI_RAT
12	27	90.0	774	1	STP_LAMBD
13	27	90.0	864	1	AGLU_MUCJA
14	27	90.0	1120	1	STRF_ECOLI
15	27	90.0	1471	1	MY84_YEAST
16	27	90.0	3344	1	POLG_PSVH
17	26	86.7	47	1	YOBP_ECOLI
18	26	86.7	148	1	YCBG_HAEIN
19	26	86.7	205	1	RAC1_DICDI
20	26	86.7	212	1	TRFP_HUMAN
21	26	86.7	212	1	TRFP_MOUSE
22	26	86.7	263	1	EXL3_ARATH
23	26	86.7	305	1	HEM3_AERPE
24	26	86.7	307	1	RUVB_MYCGE
25	26	86.7	307	1	RUVB_MYCPN
26	26	86.7	321	1	FLIM_AGR15
27	26	86.7	326	1	VT2_MXVVL
28	26	86.7	341	1	REGE_LACLA
29	26	86.7	445	1	FIBG_RAT
30	26	86.7	463	1	SYG_MYCTU
31	26	86.7	483	1	COBQ_PYRFO
32	26	86.7	496	1	ARAA_THEMEA
33	26	86.7	526	1	SYK_CHLTR

34	26	86.7	571	1	UVRC_MYCBV
35	26	86.7	611	1	ACE_HAEIE
36	26	86.7	615	1	ACE_DROME
37	26	86.7	693	1	RAP1_SCHPO
38	26	86.7	749	1	YPR2_BACSU
39	26	86.7	756	1	RPC2_MOUSE
40	26	86.7	782	1	YLIE_ECOLI
41	26	86.7	784	1	DPO2_AERPE
42	26	86.7	794	1	SYFB_THETN
43	26	86.7	901	1	VP3_BT110
44	26	86.7	901	1	VP3_BT111
45	26	86.7	901	1	VP3_BT113
46	26	86.7	901	1	VP3_BT117
47	26	86.7	901	1	VP3_BT11A
48	26	86.7	901	1	VP3_BT11S
49	26	86.7	901	1	VP3_BT12A
50	26	86.7	1133	1	RPC2_HUMAN
51	26	86.7	1135	1	RPC2_DROME
52	26	86.7	1584	1	YJ9G_YEAST
53	25	83.3	111	1	GUAV_CAVPO
54	25	83.3	147	1	LYLA_BACSU
55	25	83.3	159	1	CCME_ECOLI
56	25	83.3	259	1	TRUA_METJA
57	25	83.3	259	1	Y683_METJA
58	25	83.3	265	1	EXL1_ARATH
59	25	83.3	265	1	EXL2_ARATH
60	25	83.3	269	1	AROE_NEICI
61	25	83.3	269	1	AROE_NEIFL
62	25	83.3	269	1	AROE_NEIGO
63	25	83.3	269	1	AROE_NEIMB
64	25	83.3	269	1	AROE_NEIPO
65	25	83.3	271	1	AROE_NEIMA
66	25	83.3	297	1	YPHB_BACSU
67	25	83.3	339	1	G3P_HAEIN
68	25	83.3	346	1	MG83_HUMAN
69	25	83.3	349	1	ID12_METTH
70	25	83.3	410	1	ARCA_BORBU
71	25	83.3	444	1	TIG_MYCPN
72	25	83.3	481	1	KRL_HSV11
73	25	83.3	494	1	HEMZ_ORISA
74	25	83.3	505	1	GPMI_MYCFU
75	25	83.3	512	1	HMZ2_ARATH

ALIGNMENTS

RESULT 1  
LEC2\_MEDTR STANDARD; PRT; 280 AA.  
ID LEC2\_MEDTR  
AC Q01807;  
DT 01-JUL-1993 (Rel. 26, Created)  
DT 01-JUL-1993 (Rel. 26, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Truncated lectin 2 precursor.  
GN LEC2.

Medicago truncatula (Barrel medic).  
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae; Medicago.  
OX NCBI\_TaxID=3880;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=cv. Jemalong;  
RX MEDLINE=92379255; PubMed=1511126;  
RA Baichrowitz M.A., Barker D.G., Nadaud I., Rouge P., Lescure B.;  
RT "Lectin genes from the legume Medicago truncatula."; Plant Mol. Biol. 19:1011-1017(1992).  
CC -!- MISCELLANEOUS: LEC2 IS PROBABLY NON FUNCTIONAL, SINCE A FRAMESHIFT  
CC MUTATION LEADS TO PREMATURE TRANSLATION TERMINATION AFTER ONLY 98  
CC AA. THE SEQUENCE BELOW IGNORES THIS FRAMESHIFT MUTATION.  
CC -!- MISCELLANEOUS: BINDS ONE MANGANESE (OR OTHER TRANSITION METAL) ION  
CC AND ONE CALCIUM ION. THE METAL IONS ARE ESSENTIAL FOR THE

084898	mycoplasma
Q10715	haematobia
Q10714	drosophila
Q96t17	schizosacch
P50830	bacillus su
P59470	mus musculus
P75800	escherichia
Q83746	aeropyrum p
Q819c7	thermoanaer
P12435	bluetongue
Q65749	bluetongue
Q65750	bluetongue
P03359	bluetongue
P20608	bluetongue
P56582	bluetongue
Q65748	bluetongue
Q9nw08	homo sapien
P25167	drosophila
P47170	saccharomyc
P70107	cavia porce
Q45478	bacillus su
P33928	escherichia
Q59069	methanococc
Q58096	methanococc
Q91zt4	arabidopsis
Q9eves	arabidopsis
P95337	neisseria c
P95340	neisseria f
P95361	neisseria g
P56992	neisseria m
P56991	neisseria m
P50742	bacillus su
P44304	haemophilus
Q15480	homo sapien
Q26154	methanobact
O51781	borrelia bu
P75454	mycoplasma
P04413	herpes simp
O22101	oryza sativ
Q98qa7	mycoplasma
O04921	arabidopsis

```

CC      SACCHARIDE-BINDING AND CELL-AGGLUTININATING ACTIVITIES.
CC      -1- SIMILARITY: BELONGS TO THE LEGUMINOUS LECTIN FAMILY.
CC      -----
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CC      or send an email to license@isb-sib.ch).
CC      -----
CC      EMBL; X60387; CAA42938.1; -
CC      HSP; P04122; ILOE.
CC      InterPro; IPR000985; Lectin_legA.
CC      InterPro; IPR001220; Lectin_legB.
CC      Pfam; PF001138; lectin_legA; 1.
CC      Pfam; PF001139; lectin_legB; 1.
CC      ProDom; PD000671; Lectin_legA; 1.
CC      ProDom; PD000711; Lectin_legB; 1.
CC      PROSITE; PS00307; LECTIN_LEGUME_BETA; 1.
CC      PROSITE; PS00308; LECTIN_LEGUME_ALPHA; 1.
CC      Lectin; Manganese; Calcium; Signal; Multigene family; Glycoprotein.
CC      SIGNAL 1 26
CC      CHAIN 27 280
CC      METAL 148 148 MANGANESE (BY SIMILARITY).
CC      METAL 150 150 MANGANESE AND CALCIUM (BY SIMILARITY).
CC      METAL 152 152 CALCIUM (BY SIMILARITY).
CC      METAL 154 154 CALCIUM (BY SIMILARITY).
CC      METAL 158 158 MANGANESE AND CALCIUM (BY SIMILARITY).
CC      METAL 170 170 MANGANESE (BY SIMILARITY).
CC      CARBOHYD 163 163 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC      CARBOHYD 272 272 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC      SQ SEQUENCE 280 AA; 30473 MW; DB68690AD8015E81 CRC64;

Query Match 100.0%; Score 30; DB 1; Length 280;
Best Local Similarity 100.0%; Pred. No. 8.3;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVEY 6
Db 208 SVDVEY 213

RESULT 2
STRP_STRQ STANDARD; PRT; 440 AA.
AC P00779;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Streptokinase C precursor.
GN SKC.
OS Streptococcus equisimilis.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=119602;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H46A;
RX MEDLINE=85232082; PubMed=2989113;
RA Mulke H., Roe B., Ferretti J.J.;
RT "Nucleotide sequence of the streptokinase gene from Streptococcus
equisimilis H46A.";
RL Gene 34:357-362(1985).
RN [2]
RP SEQUENCE OF 27-440.
RX MEDLINE=83127125; PubMed=6760891;
RA Jackson K.W., Tang J.;
RT "Complete amino acid sequence of streptokinase and its homology with
serine proteases.";
RL Biochemistry 21:6620-6625(1982).
CC -1- FUNCTION: THIS PROTEIN IS NOT A PROTEASE, BUT IT ACTIVATES
PLASMINOGEN BY COMPLEXING WITH IT. AS POTENTIAL VIRULENCE FACTOR,
IT IS THOUGHT TO PREVENT THE FORMATION OF EFFECTIVE FIBRIN
BARRIERS AROUND THE SITE OF INFECTION, THEREBY CONTRIBUTING TO THE
INVASIVENESS OF THE CELLS.

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CC      IT IS THOUGHT TO PREVENT THE FORMATION OF EFFECTIVE FIBRIN
CC      BARRIERS AROUND THE SITE OF INFECTION, THEREBY CONTRIBUTING TO THE
CC      INVASIVENESS OF THE CELLS.
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CC      or send an email to license@isb-sib.ch).
CC      -----
CC      EMBL; K02986; A226974.1; -
CC      EMBL; X72832; CAA51351.1; -
CC      PIR; A22801; A22801.
CC      PDB; 1QOR; 03-MAY-00.
CC      InterPro; IPR004093; Staphylokinase.
CC      Pfam; PF02821; Staphylokinase; 3.
CC      Plasminogen activation; Signal; Virulence; 3D-structure.
CC      SIGNAL 1 26
CC      CHAIN 27 440
CC      VARIAT 195 195 STREPTOKINASE C.
CC      VARIAT 207 207 L -> D.
CC      VARIAT 298 300 D -> L.
CC      CONFLICT 298 300 EYK -> LEYK (IN REF. 2).
CC      CONFLICT 438 438 N -> D (IN REF. 2).
CC      SQ SEQUENCE 440 AA; 50140 MW; 8FC1F22648ACC77A CRC64;

Query Match 100.0%; Score 30; DB 1; Length 440;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVEY 6
Db 183 SVDVEY 188

RESULT 3
STRP_STRPY STANDARD; PRT; 440 AA.
AC P10520;
DT 01-JUL-1989 (Rel. 11, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Streptokinase A precursor.
GN SKA OR SPY1979.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1114;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SF130/13 / Serotype M1;
RX MEDLINE=89160264; PubMed=2646590;
RA Walter F., Siegel M., Mulke H.;
RT "Nucleotide sequence of the streptokinase gene from a Streptococcus
pyogenes type 1 strain.";
RL Nucleic Acids Res. 17:1261-1261(1989).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=SP370 / ATCC 700294 / Serotype M1;
RX MEDLINE=21192684; PubMed=11296296;
RA Ferretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K.,
RA Primeaux C., Szate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P.,
RA Qian Y., Jia H.G., Najjar F.Z., Ren Q., Zhu H., Song L., White J.,
RA Yuan X., Clifton S.W., Roe B.A., McLaughlin R.;
RT "Complete genome sequence of an M1 strain of Streptococcus
pyogenes.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).
CC -1- FUNCTION: THIS PROTEIN IS NOT A PROTEASE, BUT IT ACTIVATES
PLASMINOGEN BY COMPLEXING WITH IT. AS POTENTIAL VIRULENCE FACTOR,
IT IS THOUGHT TO PREVENT THE FORMATION OF EFFECTIVE FIBRIN
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CC	-----
DR	EWBL; X13399; CAA31765.1; --
DR	EWBL; AE006620; AAK34665.1; --
DR	PR; S02724; S02724.
DR	InterPro; IPR004093; Staphylokinase.
DR	Pfam; PF02821; Staphylokinase_3.
KW	Plasminogen activation; Signal; Virulence; Complete proteome.

PT	SIGNAL	1	26	
PT	CHAIN	27	440	STREPTOKINASE A.
PT	CONFLICT	163	163	L -> V (IN REP. 1).
PT	CONFLICT	345	345	R -> G (IN REP. 1).
PT	CONFLICT	373	373	D -> N (IN REP. 1).
PT	CONFLICT	428	428	D -> Y (IN REP. 1).
PT	CONFLICT	438	438	K -> N (IN REP. 1).
PT	SEQUENCE	440	440	6222EFO40B758DB CRC64:
PT	SEQUENCE	440	440	43924 MW:

Query Match	100.0%	Score 30;	DB 1;	Length 440;
Best Local Similarity	100.0%	Pred. No. 13;		
Matches	6;	Conservative	0;	Mismatches
			0;	Indels
			0;	Gaps

Qy	1	SYDVEY	6
Db	183	SYDVEY	188

RESULT 4	
STRP_STRSP	STRP_STRSP
ID	STRP_STRSP
AC	P10519;
DT	01-JUL-1989 (Rel. 11, Created)
DT	01-JUL-1989 (Rel. 11, Last sequence update)
DT	01-NOV-1997 (Rel. 35, Last annotation update)
DE	Streptokinase G precursor.

GN SKG.  
OS Streptococcus sp. (strain 19309)  
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;  
OC Streptococcus.  
OX NCBI\_TaxID=1306;  
RN [1]  
RP SEQUENCE FROM N. A.  
RX MEDLINE=89160265; PubMed=2922269;  
RA Walter F., Siegel M., Maikle H.;  
RT "Nucleotide sequence of the streptokinase gene from a group-G  
RT Streptococcus.";  
RL Nucleic Acids Res. 17:1262-1262(1989).

-!- FUNCTION: THIS PROTEIN IS NOT A PROTEASE, BUT IT ACTIVATES PLASMINOGEN BY COMPLEXING WITH IT. AS POTENTIAL VIRULENCE FACTOR, IT IS THOUGHT TO PREVENT THE FORMATION OF EFFECTIVE FIBRIN BARRIERS AROUND THE SITE OF INFECTION, THEREBY CONTRIBUTING TO THE INVASIVENESS OF THE CELLS.

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CC -----  
EMBL: X13400; CAA31766.1; -.  
PIR: S02723; S02723.  
InterPro: IPR004093; Staphylokinase.  
Pfam: PF02821; Staphylokinase; 3.  
plasminogen activation; Signal; Virulence.  
FT SIGNAL 1 26

```

FT CHAIN      27      440      STREPTOKINASE G.
SQ SEQUENCE  440 AA; 50199 MW;  5521F8825FE1B6EA CRC64;

Query Match      100.0%; Score 30; DB 1; Length 440;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy 1 SVDVEY 6  
| | | | |  
Db 183 SVDVEY 188

RESULT 5	Y34A_METJA	STANDARD;	PRT;	183 AA.
ID	Y34A_METJA			
AC	P81307;			
DT	15-JUL-1998 (Rel. 36, Created)			
DT	15-JUL-1998 (Rel. 36, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Hypothetical protein MJ0347.1.			
GN	MJ0347.1.			
OS	Methanococcus jannaschii.			
OC	Archaea; Euryarchaeota; Methanococci; Methanococcales;			
OC	Methanocaldococcaceae; Methanocaldococcus.			
OX	NCBI TaxID=2190.			

SEQUENCE FROM N.A.  
 STRAIN=JAL-1 / DSM 2661 / ATCC 43067;  
 MEDLINE=96337999; PubMed=8668087;  
 Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,  
 Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,  
 Kervilange A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,  
 Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,  
 Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrman J.L., Nguyen D.,  
 Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,  
 Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,  
 Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.:  
 "Complete genome sequence of the methanogenic archaeon, *Methanococcus*  
*jannaschii*,"  
 Science 273:1058-1073 (1996).

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DR EMBL; U67488; AAB98344.1; -.  
DR TIGR; MJ0347.1; -.  
KW Hypothetical protein; Complete proteome.  
SQ SEQUENCE 183 AA; 21756 MW; 769FCF680B86C895 CRC64;

Query Match	96.7%	Score 29;	DB 1;	Length 183;
Best Local Similarity	83.3%	Pred. No. 9.1;		
Matches 5;	Conservative 1;	Mismatches 0;	Indels 0;	Gaps 0;

Q7	1	SVDVEY 6
		:
Db	11	SVDIEY 16

**RESULT 6**

DCUP WIGBR	STANDARD;	PRT; 360 AA.
ID		
AC Q8CW15,		
DT 15-SEP-2003	(Rel. 42, Created)	
DT 15-SEP-2003	(Rel. 42, Last sequence update)	
DT 15-SEP-2003	(Rel. 42, Last annotation update)	
DE Uroporphyrinogen decarboxylase (EC 4.1.1.37) [URO-D] (UPD).		
HEME OR WIGBR5080.		
OS Wiglesworthia glossinidia brevipalpis.		



DR PRINTS; PR00747; GLYHDRLASE47.  
KW Hypothetical protein; Transport; Protein transport; Golgi stack;  
KW Membrane.  
SQ SEQUENCE 742 AA; 84075 MW; 85998EF365194E39 CRC64;  
  
Query Match 96.7%; Score 29; DB 1; Length 742;  
Best Local Similarity 83.3%; Pred. No. 41;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 SVDVEY 6  
|||:  
Db 682 SVDIEY 687  
  
RESULT 8  
DNAI BACSU STANDARD; PRT; 311 AA.  
ID AC P06567;  
DT 01-JAN-1988 (Rel. 06, Created)  
DT 01-JAN-1988 (Rel. 06, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Primosomal protein dnaI.  
GN DNAI.  
OS Bacillus subtilis.  
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
OX NCBI\_TaxID=1423;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=87117549; PubMed=3027671;  
RA Ogasawara N., Moriya S., Mazza P.G., Yoshikawa H.;  
RT "Nucleotide sequence and organization of dnaB gene and neighbouring  
genes on the Bacillus subtilis chromosome.";  
RL Nucleic Acids Res. 14:9989-9999 (1986).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX STRAIN=168;  
RA MEDLINE=97124191; PubMed=8969504;  
RA Wipat A., Carter N., Brignell C.S., Guy J.B., Piper K.,  
RA Sanders J., Emerson P.T., Harwood C.R.;  
RT "The dnaB-pheA (256 degrees-240 degrees) region of the Bacillus  
subtilis chromosome containing genes responsible for stress  
responses, the utilization of plant cell walls and primary  
metabolism.";  
RL Microbiology 142:3067-3078 (1996).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX STRAIN=168;  
RA MEDLINE=98048457; PubMed=9387221;  
RA Lapidus A., Galleron N., Sorokin A., Ehrlich S.D.;  
RT "Sequencing and functional annotation of the Bacillus subtilis genes  
in the 200 kb rnb-dnaB region.";  
RL Microbiology 143:3431-3441 (1997).  
RN [4]  
RP SEQUENCE FROM N.A.  
RX STRAIN=168;  
RA MEDLINE=98044033; PubMed=9384377;  
RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,  
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borcher S.,  
RA Borris R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,  
RA Broutlet S., Brusch C.V., Caldwell B., Capuano V., Carter N.M.,  
RA Choi S.K., Codani J.J., Conerton I.F., Cummings N.J., Daniel R.A.,  
RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,  
RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,  
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,  
RA Ghim S.Y., Glaser P., Goffeau A., Gollightly E.J., Grandi G.,  
RA Guiseppe G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,  
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,  
RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,  
RA Kobayashi Y., Koester P., Koningsstein G., Krogh S., Kumano M.,  
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,  
RA Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,  
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,  
RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,

PA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,  
RA Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,  
RA Rieger M., Rivoita C., Roche B., Roche B., Rose M., Sadale Y.,  
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,  
RA Sekiguchi J., Sekowska A., Seror S.J., Seror P., Shin B.S., Soldo B.,  
RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,  
RA Takeuchi M., Tanakoshi A., Tanaka T., Terpetra P., Tognoni A.,  
RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,  
RA Viari A., Wambutt R., Wedler E., Wedler H., Weitzenecker T.,  
RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,  
RA Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.;  
RT "The complete genome sequence of the Gram-positive bacterium Bacillus  
subtilis.";  
RL Nature 390:249-256 (1997).  
RN [5]  
RP SEQUENCE OF 1-206 FROM N.A.  
RX MEDLINE=87118226; PubMed=3027697;  
RA Hoshino T., McKenzie T., Schmidt S., Tanaka T., Sueoka N.;  
RT "Nucleotide sequence of Bacillus subtilis dnaB: a gene essential for  
DNA replication initiation and membrane attachment.";  
RL Proc. Natl. Acad. Sci. U.S.A. 84:653-657 (1987).  
RN [6]  
RP SIMILARITY TO DNAA.  
RX MEDLINE=92195821; PubMed=1549481;  
RA Koonin E.V.;  
RT "Archaeobacterial virus SSV1 encodes a putative DnaA-like protein.";  
RL Nucleic Acids Res. 20:1143-1143 (1992).  
RN [7]  
RP IDENTIFICATION.  
RX MEDLINE=95291463; PubMed=7773414;  
RA Bruand C., Ehrlich S.D.;  
RT "The Bacillus subtilis dnaI gene is part of the dnaB operon.";  
RL Microbiology 141:1199-1200 (1995).  
CC -!- FUNCTION: PROBABLY INVOLVED IN DNA REPLICATION.  
CC -!- SIMILARITY: SOME, TO DNAA FROM VARIOUS BACTERIA.  
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or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
-----  
DR EMBL; X04963; CAA28633.1; --  
DR EMBL; Z75208; CAA99605.1; --  
DR EMBL; AF008220; AAC00359.1; --  
DR EMBL; Z99118; CAB14858.1; --  
DR EMBL; M15183; AAA22405.1; --  
DR PIR; B24720; IQBS44.  
DR Subtilist; BG10359; dnaI.  
DR InterPro; IPR003593; AAA\_ATPase.  
DR SMART; SM00382; AAA; 1.  
KW Primosome; DNA replication; ATP-binding; Complete proteome.  
FT NP BIND 168 175 X -> N (IN REF. 5).  
FT CONFLICT 19 19 M -> T (IN REF. 5).  
FT CONFLICT 24 24  
SQ SEQUENCE 311 AA; 36114 MW; A86FC94AB6841264 CRC64;  
  
Query Match 93.3%; Score 28; DB 1; Length 311;  
Best Local Similarity 66.7%; Pred. No. 28;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 SVDVEY 6  
|||:  
Db 93 SVDIEY 98  
  
RESULT 9  
TPPI MOUSE STANDARD; PRT; 562 AA.  
ID TPPI\_MOUSE  
AC O89023; O89057;  
DT 15-DEC-1998 (Rel. 37, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Tripeptidyl-peptidase I precursor (EC 3.4.14.9) (TPP-I) (Tripeptidyl  
 DE aminopeptidase) (Lysosomal pepstatin insensitive protease) (LPIC).  
 GN CLN2 OR TPP1.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=99142696; PubMed=9999590;  
 RA Vines D.J., Warburton M.J.;  
 RT "Classical late infantile neuronal ceroid lipofuscinosis fibroblasts  
 RT are deficient in lysosomal tripeptidyl peptidase I.";  
 RL FEBS Lett. 443:131-135(1999).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20028316; PubMed=10556422;  
 RA Katz M.L., Liu P.-C., Grob-Nunn S.E., Shibuya H., Johnson G.S.;  
 RT "Characterization and chromosomal mapping of a mouse ortholog of the  
 RT late-infantile ceroid-lipofuscinosis gene CLN2.";  
 RL Mamm. Genome 10:1050-1053(1999).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA Sleat D.E., Lobel P.;  
 RT "Murine homologue of the lysosomal pepstatin insensitive protease  
 RT which is deficient in human classical late infantile neuronal ceroid  
 RT lipofuscinosis.";  
 RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Kidney;  
 RX MEDLINE=21085660; PubMed=11217851;  
 RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,  
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,  
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,  
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
 RA Fleischmann W., Gaasterland T., Giesi C., King B., Kochiwa H.,  
 RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,  
 RA Schrim L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,  
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,  
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,  
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,  
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,  
 RA Hayashizaki Y.;  
 RT "Functional annotation of a full-length mouse cDNA collection.";  
 RL Nature 409:685-690(2001).  
 CC -!- FUNCTION: Lysosomal serine protease with tripeptidyl-peptidase I  
 CC activity. May act as a non-specific lysosomal peptidase which  
 CC generates tripeptides from the breakdown products produced by  
 CC lysosomal proteinases. Requires substrates with an unsubstituted  
 CC N-terminus (By similarity).  
 CC -!- CATALYTIC ACTIVITY: Release of an N-terminal tripeptide from a  
 CC polypeptide, but also endopeptidase activity.  
 CC -!- SUBCELLULAR LOCATION: Lysosomal.  
 CC -!- PTM: Activated by autocatalytic proteolytical processing upon  
 CC acidification (By similarity).  
 CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S53.  
 CC  
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CC EMBL; AJ011912; CA009863.1; ALT\_INIT.  
 DR EMBL; AF124599; AAD32573.1; -  
 DR EMBL; AF111172; AAD03083.1; -  
 DR EMBL; AK002418; BAB22085.1; -  
 DR MEROPS; S53.003; -  
 DR MGD; MG1:1338194; Clin2  
 KW Hydrolyase; Protease; Serine protease; Zymogen; Signal; Lysosome;  
 KW Glycoprotein.  
 FT SIGNAL 1 19 BY SIMILARITY.  
 FT PROPEP 20 194 REMOVED IN MATURE FORM (BY SIMILARITY).  
 FT CHAIN 195 562 TRIPEPTIDYL-PEPTIDASE I.  
 FT ACT\_SITE 359 359 BY SIMILARITY.  
 FT ACT\_SITE 474 474 NUCLEOPHILE (BY SIMILARITY).  
 FT ACT\_SITE 516 516 BY SIMILARITY.  
 FT CARBOHYD 209 209 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 221 221 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 285 285 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 312 312 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 442 442 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CONFLICT 1 1 M -> V (IN REF. 1).  
 FT CONFLICT 562 562 P -> LDPFVP (IN REF. 1).  
 SQ SEQUENCE 562 AA; 61342 MW; 0AF8163EA1A66396 CRC64;  
 Query Match 90.0%; Score 27; DB 1; Length 562;  
 Best Local Similarity 83.3%; Pred. No. 91;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SVDVEY 6  
 DB 273 SLDVEY 278  
 RESULT 10  
 TPP1\_CANFA  
 ID TPP1\_CANFA STANDARD; PRT; 563 AA.  
 AC Q9XSBB;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Tripeptidyl-peptidase I precursor (EC 3.4.14.9) (TPP-I) (Tripeptidyl  
 DE aminopeptidase) (Lysosomal pepstatin insensitive protease) (LPIC).  
 GN CLN2 OR TPP1.  
 OS Canis familiaris (Dog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
 OX NCBI\_TaxID=9615;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Liu P.-C., Katz M.L., Siakotos A.N., Grob S.E., Johnson G.S.;  
 RT "Coding sequence and exon/intron organization of the canine CLN2 gene  
 RT and its exclusion as the locus for ceroid lipofuscinosis in English  
 RT setter dogs.";  
 RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: Lysosomal serine protease with tripeptidyl-peptidase I  
 CC activity. May act as a non-specific lysosomal peptidase which  
 CC generates tripeptides from the breakdown products produced by  
 CC lysosomal proteinases. Requires substrates with an unsubstituted  
 CC N-terminus (By similarity).  
 CC -!- CATALYTIC ACTIVITY: Release of an N-terminal tripeptide from a  
 CC polypeptide.  
 CC -!- SUBCELLULAR LOCATION: Lysosomal.  
 CC -!- PTM: Activated by autocatalytic proteolytical processing upon  
 CC acidification (By similarity).  
 CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S53.  
 CC  
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CC EMBL; AF114167; AAD25043.1; -.
CC MROPS; S53.003; -.
CC Hydrolase; Protease; Serine protease; Zymogen; Signal; Lysosome;
CC Glycoprotein.
CC SIGNAL 1 19 BY SIMILARITY.
CC PROPEP 20 195 REMOVED IN MATURE FORM (BY SIMILARITY).
CC CHAIN 196 563 TRIPEPTIDYL-PEPTIDASE I.
CC ACT_SITE 360 360 BY SIMILARITY.
CC ACT_SITE 475 475 NUCLEOPHILE (BY SIMILARITY).
CC ACT_SITE 517 517 BY SIMILARITY.
CC CARBOHYD 210 210 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 222 222 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 286 286 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 313 313 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 443 443 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC SEQUENCE 563 AA; 61362 MW; 2145544C34934F4 CRC64;

Query Match 90.0%; Score 27; DB 1; Length 563;
Best Local Similarity 83.3%; Pred. No. 91;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVEY 6
DB 274 SLDVEY 279

RESULT 11
TPPI_RAT
ID --TPPI_RAT STANDARD; PRT; 563 AA.
AC Q9EQV6;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Tripeptidyl-peptidase I precursor (EC 3.4.14.9) (TPP-I) (Tripeptidyl
DE aminopeptidase) (Lysosomal peptidase insensitive protease) (LPICI).
GN CLN2 OR TPPI.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Du P., Kato S., Li Y., Maeda T., Yamane T., Yamamoto S., Fujiwara M.,
RA Yamamoto Y., Nishi K., Ohkubo I.;
RT "Rat tripeptidyl peptidase I: its purification and molecular
RT cloning.";
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 196-217; 374-392 AND 395-429, AND CHARACTERIZATION.
RC TISSUE=Spleen;
RA Vines D.J., Warburton M.J.;
RA MEDLINE=98323562; PubMed=9659384;
RT "Purification and characterisation of a tripeptidyl aminopeptidase I
RT from rat spleen.";
RL Biochim. Biophys. Acta 1384:233-242(1998).
CC -1- FUNCTION: Lysosomal serine protease with tripeptidyl-peptidase I
CC activity. May act as a non-specific lysosomal peptidase which
CC generates tripeptides from the breakdown products produced by
CC lysosomal proteinases. Requires substrates with an unsubstituted
CC N-terminus. Maximum activity at pH 4, unstable above pH 7.
CC -1- CATALYTIC ACTIVITY: Release of an N-terminal tripeptide from a
CC polypeptide.
CC -1- SUBCELLULAR LOCATION: Lysosomal.
CC -1- PTM: Activated by autocatalytic proteolytical processing upon
CC acidification (By similarity).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S53.
CC
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CC or send an email to licenses@isb-sib.ch).
CC
CC EMBL; AB043870; BAB18570.1; -.
CC Hydrolase; Protease; Serine protease; Zymogen; Signal; Lysosome;
CC Glycoprotein.
CC SIGNAL 1 19 BY SIMILARITY.
CC PROPEP 20 195 REMOVED IN MATURE FORM.
CC CHAIN 196 563 TRIPEPTIDYL-PEPTIDASE I.
CC ACT_SITE 360 360 BY SIMILARITY.
CC ACT_SITE 475 475 NUCLEOPHILE (BY SIMILARITY).
CC ACT_SITE 517 517 BY SIMILARITY.
CC CARBOHYD 210 210 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 222 222 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 286 286 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 313 313 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 443 443 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CONFLICT 210 210 N -> A (IN REF. 2).
CC CONFLICT 216 217 VG -> SQ (IN REF. 2).
CC CONFLICT 389 391 GGT -> SPP (IN REF. 2).
CC SEQUENCE 563 AA; 61332 MW; B54F3C86205DFEC1 CRC64;

Query Match 90.0%; Score 27; DB 1; Length 563;
Best Local Similarity 83.3%; Pred. No. 91;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVEY 6
DB 274 SLDVEY 279

RESULT 12
STP_LAMBDA
ID STP_LAMBDA STANDARD; PRT; 774 AA.
AC P03764; P03745;
DT 21-JUL-1986 (Rel. 01, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Side tail fiber protein.
GN STP.
OS Bacteriophage lambda.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;
OC Lambda-like viruses.
OX NCBI_TaxID=10710;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=83189071; PubMed=6221115;
RA Sanger F., Coulson A.R., Hong G.F., Hill D.F., Petersen G.B.;
RT "Nucleotide sequence of bacteriophage lambda DNA.";
RL J. Mol. Biol. 162:729-773(1982).
RN [2]
RP IDENTIFICATION AS STP.
RX MEDLINE=92165720; PubMed=1531648;
RA Hagsaard-Ljungquist E., Halling C., Calendar R.;
RT "DNA sequences of the tail fiber genes of bacteriophage P2: evidence
RT for horizontal transfer of tail fiber genes among unrelated
RT bacteriophages.";
RL J. Bacteriol. 174:1462-1477(1992).
RN [3]
RP RECONSTRUCTION.
RX MEDLINE=93068310; PubMed=1439823;
RA Hendrix R.W., Duda R.L.;
RT "Bacteriophage lambda Papa: not the mother of all lambda phages.";
RL Science 258:1145-1148(1992).
CC -1- MISCELLANEOUS: The common laboratory strain of bacteriophage
CC lambda; lambda Papa; carries a frameshift mutation relative to Ur-
CC lambda, the original isolate. The Ur-lambda virions have thin,
CC jointed tail fibers (side tail fibers) that are absent from lambda
CC wild type. Relative to lambda Papa, Ur-lambda has expanded
CC receptor specificity and adsorbs to E.coli cells more rapidly.
CC -1- SIMILARITY: BELONGS TO THE TAIL FIBER FAMILY.
CC -1- CAUTION: THIS IS A CONCEPTUAL TRANSLATION; A FRAMESHIFT WAS

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CC CORRECTED IN POSITION TO 396 TO RECREATE THE ORIGINAL STF PROTEIN.  
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CC -----  
CC EMBL; J02459; AAA96555.1; ALT\_FRAME.  
CC EMBL; J02459; AAA96557.1; ALT\_FRAME.  
CC PIR; C43009; QXEP21.  
CC InterPro; IPR005003; Phage\_fiber.  
CC InterPro; IPR005068; Phage\_fiber\_2.  
CC Pfam; PF03335; Phage\_fiber; 6.  
CC Pfam; PF03406; Phage\_fiber\_2; 1.  
CC Fiber protein.  
KW Fiber protein.  
SQ SEQUENCE 774 AA; 77527 MW; CDDIDF85E919123B CRC64;  
  
Query Match 90.0%; Score 27; DB 1; Length 774;  
Best Local Similarity 83.3%; Pred. No. 1.3e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 SVDVEY 6  
DB 50 SMDVEY 55  
:|||||  
|:|||||  
  
RESULT 13  
AGLU\_MUCJA STANDARD; PRT; 864 AA.  
ID AGLU\_MUCJA  
AC Q92442;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Alpha-glucosidase precursor (EC 3.2.1.20) (Maltase).  
OS Mucor javanicus.  
OC Eukaryota; Fungi; Zygomycota; Zygomycetes; Mucorales; Mucoraceae;  
OC Mucor.  
OX NCBI\_TaxID=51122;  
RN [1]  
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.  
RC STRAIN=IFO 4570;  
RX MEDLINE=96271012; PubMed=8830045;  
RA Sugimoto M., Suzuki Y.;  
RT "Molecular cloning, sequencing, and expression of a cDNA encoding  
RT alpha-glucosidase from Mucor javanicus";  
RL J. Biochem. 119:500-505 (1996).  
CC -!- FUNCTION: Hydrolyzes not only malto-oligosaccharides but also  
CC soluble starch.  
CC -!- CATALYTIC ACTIVITY: Hydrolysis of terminal, non-reducing 1,4-  
CC linked D-glucose residues with release of D-glucose.  
CC -!- SIMILARITY: BELONGS TO FAMILY 31 OF GLYCOSYL HYDROLASES.  
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CC -----  
CC EMBL; D67034; BAA11053.1; -  
CC InterPro; IPR000322; Glyco\_hydro\_31.  
CC Pfam; PF01055; Glyco\_hydro\_31; 1.  
CC PROSITE; PS00129; GLYCOSYL HYDROL\_F31\_1; 1.  
CC PROSITE; PS00707; GLYCOSYL HYDROL\_F31\_2; FALSE\_NEG.  
KW Hydrolase; Glycosidase; Glycoprotein; Signal.  
FT SIGNAL 1 22 POTENTIAL.  
FT CHAIN 23 864 ALPHA-GLUCOSIDASE.  
FT ACT\_SITE 430 430 BY SIMILARITY.  
FT CARBOHYD 187 187 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT

FT CARBOHYD 364 364 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 406 406 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 466 466 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 500 500 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 568 568 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 734 734 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 864 AA; 98761 MW; CFAB4759DC431403 CRC64;  
  
Query Match 90.0%; Score 27; DB 1; Length 864;  
Best Local Similarity 83.3%; Pred. No. 1.4e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 SVDVEY 6  
DB 75 TVDVEY 80  
:|||||  
|:|||||  
  
RESULT 14  
STPR\_ECOLI STANDARD; PRT; 1120 AA.  
ID STPR\_ECOLI  
AC P76072; P77560;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Side tail fiber protein homolog from lambdoid prophage Rac.  
GN STPR OR B1372.  
OS Escherichia coli.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Escherichia.  
OX NCBI\_TaxID=562;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=K12 / MG1655;  
RX MEDLINE=97426617; PubMed=9278503;  
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,  
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,  
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,  
RA Mau B., Shao Y.;  
RT "The complete genome sequence of Escherichia coli K-12";  
RL Science 277:1453-1474 (1997).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=K12;  
RX MEDLINE=97251357; PubMed=9097039;  
RA Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Itoh T.,  
RA Kasai H., Kashimoto K., Kimura S., Kitakawa M., Kitagawa M.,  
RA Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,  
RA Nakade S., Nakamura Y., Nashimoto H., Nishio Y., Oshima T., Saito N.,  
RA Sampei G., Seki Y., Sivasubram S., Tagami H., Takeda J.,  
RA Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horiuchi T.;  
RT "A 570-kb DNA sequence of the Escherichia coli K-12 genome  
RT corresponding to the 28.0-40.1 min region on the linkage map";  
RL DNA Res. 3:363-377 (1996).  
CC -!- SIMILARITY: BELONGS TO THE TAIL FIBER FAMILY.  
CC -----  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
CC EMBL; AE000234; AAC74454.1; ALT\_INIT.  
CC EMBL; D90774; BAA14966.1; -  
CC EMBL; D90775; BAA14975.1; -  
CC PIR; G64887; G64887.  
CC EcoGene; EG13370; stfR.  
CC InterPro; IPR005003; Phage\_fiber.  
CC InterPro; IPR005068; Phage\_fiber\_2.  
CC Pfam; PF03335; Phage\_fiber; 6.  
CC Pfam; PF03406; Phage\_fiber\_2; 1.  
KW Hypothetical protein; Fiber protein; Repeat; Complete proteome.



```
SQ SEQUENCE 1120 AA; 113779 MW; 542E59D71EE795B4 CRC64;
Query Match 90.0%; Score 27; DB 1; Length 1120;
Best Local Similarity 83.3%; Pred. No. 1.9e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVEY 6
Db 50 SMDVEY 55

RESULT 15
MYSA4 YEAST
ID MYSA4 YEAST STANDARD; PRT; 1471 AA.
AC P32432;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE MYOSIN-4 isoform.
GN MYO4 OR SHE1 OR YAL029C OR FUN22.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94334370; PubMed=8056830;
RA Haarer B.K., Petzold A., Lillie S.H., Brown S.S.;
RT "Identification of MYO4, a second class V myosin gene in yeast.";
RL J. Cell Sci. 107:1055-1064(1994).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=9288C / AB972;
RX MEDLINE=95249563; PubMed=7731988;
RA Bussey H., Kaback D.B., Zhong W., Vo D.T., Clark M.W., Fortin N.,
RA Hall J., Ouellette B.F.F., Keng T., Barton A.B., Su Y., Davies C.K.,
RA Storms R.K.;
RT "The nucleotide sequence of chromosome I from Saccharomyces
RT cerevisiae.";
RL Proc. Natl. Acad. Sci. U.S.A. 92:3809-3813(1995).
CC -1- FUNCTION: SEEMS TO BE RESPONSIBLE FOR THE ACCUMULATION IN DAUGHTER
CC CELLS OF ASH1, A REPRESSOR OF THE HO ENDONUCLEASE.
CC -1- SUBCELLULAR LOCATION: ACCUMULATES PREFERENTIALLY IN GROWING BUDS.
CC -1- SIMILARITY: Contains 1 myosin-like globular head domain.
CC -1- SIMILARITY: Contains 1 dilute domain.
CC -1- SIMILARITY: Contains 5 IQ domains.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to licenses@isb-sib.ch).
CC -----
DR ENBL; M90057; AAC37409.1; -;
DR ENBL; U12980; AAC05003.1; -;
DR PIR; S30790; S30790.
DR HSSP; P10587; 1BR2.
DR SGD; S0000027; MYO4.
DR GO; GO:0000143; C-actin cap (sensu Saccharomycetes); IDA.
DR InterPro; IPR002710; DIL.
DR InterPro; IPR000048; IQ_region.
DR InterPro; IPR001609; myosin_head.
DR InterPro; IPR004009; Myosin_N.
DR Pfam; PF01843; DIL; 1.
DR Pfam; PF00612; IQ; 5.
DR Pfam; PF00063; myosin_head; 1.
DR Pfam; PF02736; Myosin_N; 1.
DR PRINTS; PR00193; MYOSINHEAVY.
DR ProDom; PD000355; myosin_head; 1.
DR SMART; SM00015; IQ; 2.
DR SMART; SM00242; MYSC; 1.
```

```
DR PROSITE; PS00096; IQ; 2.
KW Myosin; ATP-binding; Actin-binding; Calmodulin-binding; Repeat;
FT Coiled coil; Alkylation.
FT DOMAIN 1 777 MYOSIN HEAD-LIKE.
FT DOMAIN 781 801 IQ 1.
FT DOMAIN 804 824 IQ 2.
FT DOMAIN 829 849 IQ 3.
FT DOMAIN 876 898 IQ 4.
FT DOMAIN 899 928 IQ 5.
FT DOMAIN 938 1063 COILED COIL.
FT DOMAIN 1299 1401 DILUTE.
FT NP_BIND 165 172 ATP (POTENTIAL).
FT MOD_RES 688 688 ALKYLATION (BY SIMILARITY).
FT MOD_RES 698 698 ALKYLATION (BY SIMILARITY).
SQ SEQUENCE 1471 AA; 169343 MW; E79C0FE72B041E95 CRC64;

Query Match 90.0%; Score 27; DB 1; Length 1471;
Best Local Similarity 83.3%; Pred. No. 2.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVEY 6
Db 568 AVDEY 573

RESULT 16
POLG PRSVH
ID POLG PRSVH STANDARD; PRT; 3344 AA.
AC Q01901;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Genome polyprotein [Contains: N-terminal protein (P1); Helper
DE component proteinase (EC 3.4.22.45) (HC-Pro); Protein P3; 6 kDa
DE protein 1 (6k1); Cytoplasmic inclusion protein (CI); 6 kDa protein 2
DE (6k2); Genome-linked protein (VPG); Nuclear inclusion protein A (NI-A)
DE (NIA) (EC 3.4.22.44) (49 kDa proteinase) (49 kDa-Pro); Nuclear
DE inclusion protein B (NI-B) (NIB) (RNA-directed RNA polymerase)
DE (EC 2.7.7.48); Coat protein (CP)].
OS Papaya ringspot virus (strain P / mutant HA).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;
OC Potyvirus.
OX NCBI_TaxID=31731;
RN [1]
RP SEQUENCE FROM N.A.
RA Wang C.H., Bau H.J., Yeh S.D.;
RT "Comparison of the nuclear inclusion b protein and coat protein genes
RT of five papaya ringspot virus strains distinct in geographic origin
RT and pathogenicity.";
RL Phycopathology 84:1205-1210(1994).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=93019006; PubMed=1402799;
RA Yeh S.D., Jan F.J., Chiang C.H., Doong T.J., Chen M.C.,
RA Chung P.H., Bau H.J.;
RT "Complete nucleotide sequence and genetic organization of papaya
RT ringspot virus RNA.";
RL J. Gen. Virol. 73:2531-2541(1992).
RN [3]
RP SEQUENCE OF 2561-3344 FROM N.A.
RX MEDLINE=93090098; PubMed=1458896;
RA Wang C.H., Yeh S.D.;
RT "Nucleotide sequence comparison of the 3'-terminal regions of severe,
RT mild, and non-papaya infecting strains of papaya ringspot virus.";
RL Arch. Virol. 127:345-354(1992).
CC -1- FUNCTION: HELPER COMPONENT-PROTEINASE IS REQUIRED FOR APHID
CC TRANSMISSION AND ALSO HAS PROTEOLYTIC ACTIVITY.
CC -1- FUNCTION: CYTOPLASMIC INCLUSION PROTEIN HAS HELICASE ACTIVITY. IT
CC MAY BE INVOLVED IN REPLICATION.
CC -1- FUNCTION: NUCLEAR INCLUSION PROTEIN A HAS PROTEOLYTIC ACTIVITY.
CC -1- CATALYTIC ACTIVITY: Hydrolyzes glutamyl bonds, and activity is
CC further restricted by preferences for the amino acids in P6 - P1,
CC that vary with the species of potyvirus, e.g. Glu-Xaa-Xaa-Tyr-Xaa-
```

Gln+(Ser or Gly) for the enzyme from tobacco etch virus. The natural substrate is the viral polyprotein, but other proteins and oligopeptides containing the appropriate consensus sequence are also cleaved.

-/- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate + {RNA} (N).

-/- CATALYTIC ACTIVITY: Hydrolyzes a Gly-|-Gly bond at its own C-terminus, commonly in the sequence -Tyr-Xaa-Val-Gly-|-Gly, in the processing of the polyviral polyprotein.

-/- PPM: VPG IS COVALENTLY LINKED TO THE GENOMIC RNA.

-/- PPM: THE VIRAL RNA OF POLYVIRUSES IS EXPRESSED AS A SINGLE POLYPROTEIN WHICH UNDERGOES POSTTRANSLATIONAL PROTEOLYTIC PROCESSING RESULTING IN THE PRODUCTION OF AT LEAST EIGHT INDIVIDUAL PROTEINS.

-/- SIMILARITY: HC PROTEINASE BELONGS TO PEPTIDASE FAMILY C6.

-/- SIMILARITY: NI-A PROTEINASE BELONGS TO PEPTIDASE FAMILY C4.

-/- SIMILARITY: BELONGS TO THE POTVIRUSES POLYPROTEIN FAMILY.

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EMBL: X67673; CAA47905.1; -  
 EMBL: S45722; AB23789.1; -  
 EMBL: X67672; CAA47904.1; -  
 PIR: JQ1899; JQ1899.  
 MEROPS: C04.009; -  
 MEROPS: C06.001; -  
 MEROPS: S30.001; -  
 InterPro: IPR001410; DEAD.  
 InterPro: IPR001650; Helicase\_C.  
 InterPro: IPR001730; Peptidase\_C4.  
 InterPro: IPR001456; Peptidase\_C6.  
 InterPro: IPR001592; Poty\_coat.  
 InterPro: IPR002540; Poty\_P1.  
 InterPro: IPR007095; RNA\_pol\_DS\_PS.  
 InterPro: IPR001205; RNA\_pol\_P3D.  
 InterPro: IPR007094; RNA\_pol\_PSVir.  
 Pfam: PF00271; helicase\_C\_1.  
 Pfam: PF00863; Peptidase\_C4; 1.  
 Pfam: PF00851; Peptidase\_C6; 1.  
 Pfam: PF00767; Poty\_coat; 1.  
 Pfam: PF01577; Poty\_P1; 1.  
 Pfam: PF00680; RNA\_dep\_RNA\_pol; 1.  
 PRINTS: PR00966; NTAPOTYPTASE.  
 SMART: SM00487; DEXDC; 1.  
 SMART: SM00490; HELIC; 1.  
 KW Hydrolase; Transferase; Thiol protease; RNA-directed RNA polymerase;  
 KW Coat protein; Polyprotein; Covalent protein-RNA linkage; Helicase;  
 KW ATP-binding.  
 FT CHAIN 1 529 N-TERMINAL PROTEIN (BY SIMILARITY).  
 FT CHAIN 530 1149 HELPER COMPONENT PROTEINASE  
 FT CHAIN 1150 ?  
 FT CHAIN ? 1401 PROTEIN P3 (BY SIMILARITY).  
 FT CHAIN 1402 2036 6 kDa PROTEIN 1 (BY SIMILARITY).  
 FT CHAIN 2037 2093 CYTOPLASMIC INCLUSION PROTEIN (BY  
 FT CHAIN 2094 ? SIMILARITY).  
 FT CHAIN ? 2520 6 kDa PROTEIN 2 (BY SIMILARITY).  
 FT CHAIN 2521 3037 GENOME-LINKED PROTEIN (BY SIMILARITY).  
 FT CHAIN 3038 ? NUCLEAR INCLUSION PROTEIN A  
 FT CHAIN 2156 ? (BY SIMILARITY).  
 FT CHAIN 2521 3037 NUCLEAR INCLUSION PROTEIN B  
 FT CHAIN 3038 ? (BY SIMILARITY).  
 FT CHAIN 2156 COAT PROTEIN (BY SIMILARITY).  
 FT BINDING 1486 1493 COVALENT LINKAGE OF VIRAL RNA (BY  
 FT BINDING 3344 AA; 381040 MW; E90CD7523AC5243D CRC64;  
 SQ SEQUENCE

Query Match 90.0%; Score 27; DB 1; Length 3344;  
 Best Local Similarity 83.3%; Pred. No. 6.1e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVEY 6  
 DB 149 SVDLEY 154  
 |||:|

RESULT 17  
 YOBP\_ECOLI  
 ID YOBP\_ECOLI STANDARD; PRT; 47 AA.  
 AC P76265;  
 DT 15-JUL-1999 (Rel. 38, Created)  
 DT 15-JUL-1999 (Rel. 38, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Hypothetical protein yobp.  
 GN YOBP OR B1824 OR C2232 OR Z2869 OR ECS2534 OR SF1402.  
 OS Escherichia coli O6.  
 OS Escherichia coli O157:H7, and  
 OS Shigella flexneri.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Escherichia.  
 OC NCBI TaxID=562, 217992, 83334, 623;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=E.coli; STRAIN=K12 / MG1655;  
 RX MEDLINE=97426617; PubMed=9278503;  
 RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,  
 RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,  
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,  
 RA Mau B., Shao Y.;  
 RT "The complete genome sequence of Escherichia coli K-12."  
 RL Science 277:1453-1474(1997).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=E.coli; STRAIN=O6:H1 / CFT073 / ATCC 700928;  
 RX MEDLINE=2238234; PubMed=12471157;  
 RA Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,  
 RA Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,  
 RA Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,  
 RA Mobley H.L.T., Donnenberg M.S., Blattner F.R.;  
 RT "Extensive mosaic structure revealed by the complete genome sequence  
 of uropathogenic Escherichia coli."  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=E.coli; STRAIN=O157:H7 / EDL933 / ATCC 700927;  
 RX MEDLINE=21074935; PubMed=11206551;  
 RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,  
 RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,  
 RA Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,  
 RA Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamocous K.,  
 RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,  
 RA Welch R.A., Blattner F.R.;  
 RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7."  
 RL Nature 409:529-533(2001).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=E.coli; STRAIN=O157:H7 / RIMD 0509952;  
 RX MEDLINE=21156231; PubMed=11258796;  
 RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,  
 RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,  
 RA Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,  
 RA Kuhara S., Shiba T., Hattori M., Shinagawa H.;  
 RT "Complete genome sequence of enterohaemorrhagic Escherichia coli  
 O157:H7 and genomic comparison with a laboratory strain K-12."  
 RL DNA Res. 8:11-22(2001).  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=S.flexneri; STRAIN=301 / Serotype 2a;  
 RX MEDLINE=22272406; PubMed=12384590;

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EMBL: U32811; AAC22968.1; -  
DR PIR, H64025; H64025.  
DR TIGR, H1323; -  
KW Hypothetical protein; Complete proteome.  
SQ SEQUENCE 148 AA; 17997 MW; F400CFE7A4958314 CRC64;

Query Match 86.7%; Score 26; DB 1; Length 148;  
Best Local Similarity 86.7%; Pred. No. 38;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVEY 6  
|:|:|  
Db 93 SIDLEY 98

RESULT 19  
RACI DICDI  
ID RACI DICDI STANDARD; PRT; 205 AA.  
AC QSGPR2; AC  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE RAS-related protein raci.  
GN RACI.  
OS Dictyostelium discoideum (Slime mold).  
OC Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.  
NCBI\_TaxID=44689;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=AX4;  
RX MEDLINE=21127961; PubMed=11222756;  
RT Rivero F., Dislich H., Glockner G., Noegel A.A.;  
RA "The Dictyostelium discoideum family of Rho-related proteins.";  
RL Nucleic Acids Res. 29;1068-1079(2001).  
CC -1- SIMILARITY: BELONGS TO THE SMALL GTPASE SUPERFAMILY. RHO FAMILY.  
CC  
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EMBL: AF310895; AAG45138.1; -  
DR HSSP; P15154; 1E96  
DR DictyDb; DB27777; racI.  
DR InterPro; IPR003578; GTPase\_Rho.  
DR InterPro; IPR001806; Ras\_trnsfrmg.  
DR InterPro; IPR005225; Small\_GTP.  
DR Pfam; PF00071; ras; 1.  
DR SMART; SM00174; RHO; 1.  
DR TIGRfam; TIGR00231; small\_GTP; 1.  
KW GTP-binding; Prenylation; Lipoprotein.  
FT NP\_BIND 12 19 GTP (BY SIMILARITY).  
FT FT NP\_BIND 59 63 GTP (BY SIMILARITY).  
FT FT NP\_BIND 119 122 GTP (BY SIMILARITY).  
FT FT DOMAIN 34 42 EFFECTOR REGION (POTENTIAL).  
FT FT LIPID 202 202 GERANYL-GERANYL (BY SIMILARITY).  
SQ SEQUENCE 205 AA; 22997 MW; F9EFD3A1576C45CC CRC64;

Query Match 86.7%; Score 26; DB 1; Length 205;  
Best Local Similarity 86.7%; Pred. No. 54;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVEY 6  
|:|:|  
Db 43 SLDIEY 48

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RESULT 20
TRFP HUMAN
ID TRFP_HUMAN STANDARD; PRT; 212 AA.
AC Q9H944; Q95821; Q9Y429;
DT 15-SEP-2003 (Rel. 42, Created)
DT 15-SEP-2003 (Rel. 42, Last sequence update)
DE TRF-proximal protein homolog.
GN TRFP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99134313; PubMed=9933582;
RA Xiao H., Tao Y., Roeder R.G.;
RT "The human homologue of Drosophila TRF-proximal protein is associated
RT with an RNA polymerase II-SRB complex.";
RL J. Biol. Chem. 274:3937-3940(1999).
RN [2]
RP SEQUENCE FROM N.A.
RA Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
RA Watanabe M., Hosoi T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,
RA Watanabe S., Kimura K., Murakami K., Iehil S., Kawai Y., Saito K.,
RA Yamamoto J., Wakamatsu A., Nakamura Y., Nagahara K., Masuho Y.,
RA Ninomiya K., Iwayanagi T.;
RT "NED0 human cDNA sequencing project.";
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Jatktenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toehiyuki S., Carninci P., Prange C.,
RA Raha S.S., Iqbalano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McWay P.C., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.J., Hale S., Garcia A.M., Gay L.J., Huijyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [4]
RP SEQUENCE OF 120-212 FROM N.A.
RC TISSUE=Uterus;
RA Angorse W., Winkler U., Wewes H.-W., Gassenhuber J., Wiemann S.;
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: May regulate transcription of class II genes through
CC association with the RNA polymerase II-SRB complex.
CC -!- SUBUNIT: Component of an RNA polymerase II-SRB complex.
CC -!- SUBCELLULAR LOCATION: Nuclear (Probable).
CC
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CC
CC EMBL; AF097725; AAD16169.1; -
CC EMBL; AK023092; BAB14399.1; -
CC EMBL; BC040950; AAH40950.1; -
CC EMBL; AL050196; CAB43314.1; -
CC GO; GO:0016251; F:general RNA polymerase II transcription factor; TAS.
CC GO; GO:0005515; F:protein binding; TAS.
CC GO; GO:0006357; P:regulation of transcription from Pol II pro. .; TAS.
KW Transcription regulation; Nuclear protein.
FT CONFLICT 134 136 SAR -> VP (IN REF. 1).
FT CONFLICT 206 207 MISSING (IN REF. 1).
SQ SEQUENCE 212 AA; 23222 MW; 5AA7A39981EB1498 CRC64;

Query Match 86.7%; Score 26; DB 1; Length 212;
Best Local Similarity 83.3%; Pred No. 56;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVEY 6
Db 139 SVEVEY 144

RESULT 21
TRFP MOUSE
ID TRFP_MOUSE STANDARD; PRT; 212 AA.
AC Q9R0X0;
DT 15-SEP-2003 (Rel. 42, Created)
DT 15-SEP-2003 (Rel. 42, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE TRF-proximal protein homolog.
GN TRFP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Crowley T.B.;
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6J; TISSUE=Cerebellum;
RA MEDLINE=22354683; PubMed=12468851;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaudo I., Oatuo N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schimi L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusci V., Chothia C., Corbani L.E., Cousins S.,
RA Dalia E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Perlea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Sulcano R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlstedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang L., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Iehil Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sasaki K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
CC -!- FUNCTION: May regulate transcription of class II genes through
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CC association with the RNA polymerase II-SRB complex (By
CC similarity).
CC -!- SUBUNIT: Component of an RNA polymerase II-SRB complex (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Nuclear (Probable).
CC
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CC
CC EMBL; AJ245617; CAB53514.1; -
CC DR EMBL; AK043396; BAC31536.1; -
CC DR MGI; MGI.1929648; Trfp.
CC KW Transcription regulation; Nuclear protein.
CC SQ SEQUENCE 212 AA; 23192 MW; 88E116DOA9764438 CRC64;

Query Match      86.7%; Score 26; DB 1; Length 212;
Best Local Similarity 83.3%; Pred. No. 56;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVDVEY 6
Db 139 SVEVEY 144

RESULT 22
EXL3 ARATH STANDARD; PRT; 263 AA.
AC Q9LZT5;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE Expansin-like 3 precursor (At-EXPL3) (Ath-ExpBeta-2.3).
GN EXPL3 OR AT3G45960 OR F16L2.170.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OC
CX NCBI_TaxID=3702;
RN 1
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=21016720; PubMed=11130713;
RA Salanoubat M., Lemcke K., Rieger M., Ansoerge W., Unseld M.,
RA Fartmann B., Valle G., Bloeker H., Perez-Alonso M., Obermaier B.,
RA Dalseny M., Boutry M., Grivell L.A., Mache R., Puigdomenech P.,
RA De Simone V., Choisme N., Attiguenave F., Robert C., Brottier P.,
RA Wincker P., Catolico L., Weissenbach J., Saurin W., Quetier F.,
RA Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Benes V.,
RA Wurmbach E., Drzonek H., Erfle H., Jordan N., Bangert S.,
RA Wiedelmann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G.,
RA Vezzi A., D'Angelo M., Pallavicini A., Toppo S., Simonati B.,
RA Conrad A., Hornischer K., Kauer G., Loehner T.-H., Nordstiek G.,
RA Reichelt J., Scharfe M., Schoen O., Bargues M., Terol J., Climent J.,
RA Navarro P., Collado C., Perez-Perez A., Ottenwaelder B., Duchemin D.,
RA Cooke R., Laudie M., Berger-Llauro C., Purnelle B., Masny D.,
RA De Haan M., Maarse A.C., Alcaraz J.-P., Cottet A., Casasuberta E.,
RA Monfort A., Ardirou A., Flores M., Liguori R., Vitale D.,
RA Mannhaupt G., Haase D., Schoof H., Rued S., Zaccaria P., Mewes H.-W.,
RA Mayer K.F.X., Kaul S., Town C.D., Koo H.L., Tallon L.J., Jenkins J.,
RA Rooney T., Rizzo M., Walts A., Utterback T., Fujii C.Y., Shea T.P.,
RA Creasy T.H., Haas B., Maiti R., Wu D., Peterson J., Van Aken S.,
RA Pai G., Militscher J., Sellers P., Gill J.E., Feldblyum T.V.,
RA Preuss D., Lin X., Niernan W.C., Salzberg S.B., White C., Venter J.C.,
RA Fraser C.M., Kaneko T., Nakamura Y., Sato S., Kato T., Asamizu E.,
RA Sasamoto S., Kimura T., Idesawa K., Kawashima K., Kishida Y.,
RA Kiyokawa S., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
RA Nakayama S., Nakazaki N., Shingo S., Takeuchi C., Wada T.,
RA Watanabe A., Yamada M., Yasuda M., Tabata S.;

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RT "sequence and analysis of chromosome 3 of the plant Arabidopsis
RT thaliana.";
RL Nature 408:820-822(2000).
CC -!- SIMILARITY: BELONGS TO THE EXPANSIN FAMILY.
CC -!- SIMILARITY: Contains 1 expansin-like EG45 domain.
CC -!- SIMILARITY: Contains 1 expansin-like CBD domain.
CC -!- DATABASE: NAME=EXPANSIN homepage;
CC WWW="http://www.bio.psu.edu/expansins/".
CC
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CC
CC EMBL; AL162459; CAB82820.1; -
CC DR EMBL; T47536; T47536.
CC DR InterPro; IPR007112; Expan_endogl.
CC DR InterPro; IPR007118; Expan_Lol_pi.
CC DR InterPro; IPR007117; Expan_Lol_pi_C.
CC DR Pfam; PF01357; Pollen_allergen; 1.
CC DR PRINTS; PR01225; EXPANSNFAMLY.
CC DR PRODom; PD002179; Expan_Lol_pi_C; 1.
CC DR PROSITE; PS50843; EXPANSIN_CBD; 1.
CC DR PROSITE; PS50842; EXPANSIN_EG45; 1.
CC KW Glycoprotein; Signal; Multigene family.
CC FT SIGNAL 1 20 POTENTIAL.
CC FT CHAIN 21 263 EXPANSIN-LIKE 3.
CC FT DOMAIN 41 147 EXPANSIN-LIKE EG45.
CC FT DOMAIN 161 243 EXPANSIN-LIKE CBD.
CC FT CARBOHYD 99 99 N-LINKED (GLCNAC. .) (POTENTIAL).
CC FT CARBOHYD 102 102 N-LINKED (GLCNAC. .) (POTENTIAL).
CC SQ SEQUENCE 263 AA; 28559 MW; 5D8A2048FEA7C292 CRC64;

Query Match      86.7%; Score 26; DB 1; Length 263;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VDVEY 6
Db 133 VDVEY 137

RESULT 23
HEM3 AERPE
ID HEM3 AERPE STANDARD; PRT; 305 AA.
AC Q9Y9J0;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Probable porphobilinogen deaminase (EC 4.3.1.8) (PBG)
DE (Hydroxymethylbilane synthase) (HMBS) (Pre-uroporphyrinogen synthase).
DE HEMC OR APE2298.
GN Aeropyrum pernix.
OS Aeropyrum pernix.
OC Archaea; Crenarchaeota; Thermoprotei; Desulfurococcales;
OC Desulfurococaceae; Aeropyrum.
CX NCBI_TaxID=56636;
RN 1
RP SEQUENCE FROM N.A.
RC STRAIN=K1;
RX MEDLINE=99310339; PubMed=10382966;
RA Kavarabayasi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Y.,
RA Jinno K., Takahashi M., Sekine M., Baba S.-I., Ankael A., Kosugi H.,
RA Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H.,
RA Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y.,
RA Yamazaki J., Kishida N., Oguchi A., Aoki K.-I., Kubota K.,
RA Nakamura Y., Nomura N., Sako Y., Kikuchi H.;
RA "Complete genome sequence of an aerobic hyper-thermophilic
RA crenarchaeon, Aeropyrum pernix K1.";
RA DNA Res. 6:83-101(1999).
CC -!- FUNCTION: TETRAPOLYMERIZATION OF THE MONOPYRROLE PBG INTO THE

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CC HYDROXYMETHYLBILANE PREUROPORPHYRINOGEN IN SEVERAL DISCRETE STEPS.
CC -1- CATALYTIC ACTIVITY: 4 porphobilinogen + H(2)O =
CC hydroxymethylbilane + 4 NH(3).
CC -1- COFACTOR: COVALENTLY BINDS A DIPHYROMETHANE COFACTOR TO WHICH THE
CC PORPHOBILINOGEN SUBUNITS ARE ADDED (BY SIMILARITY).
CC -1- PATHWAY: Porphyrin biosynthesis by the C5 pathway; fourth step.
CC -1- SIMILARITY: BELONGS TO THE HMBS FAMILY.
CC -----
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CC -----
CC EMBL; AP000064; BA881310.1; -.
CC PIR; F72456; F72456.
CC HSSP; P06983; IPDA.
CC HAMAP; MF 00260; -. 1.
CC InterPro; IPR000860; Porphobil deam.
CC Pfam; PF01379; Porphobil deam; 1.
CC Pfam; PF03900; Porphobil deamC; 1.
CC PRINTS; PR00151; PORPHBDMNASE.
CC ProDom; PD02745; Porphobil deam; 1.
CC PROSITE; PS00533; PORPHOBILINOGEN DEAM; 1.
CC Porphyryrin biosynthesis; Lyase; Complete proteome.
KW Porphyryrin biosynthesis; Lyase; PYRROMETHANE COFACTOR (BY SIMILARITY).
FT BINDING 238 238 PYRROMETHANE COFACTOR (BY SIMILARITY).
SQ SEQUENCE 305 AA; 33085 MW; 57C78EB934C2799B CRC64;

Query Match 86.7%; Score 26; DB 1; Length 305;
Best Local Similarity 100.0%; Pred. No. 83;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDVEY 6
DB 177 VDVEY 181

RESULT 24
RUVB_MYCGE STANDARD; PRT; 307 AA.
AC Q49425;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Holliday junction DNA helicase ruvb.
GN RUVB OR MG359.
OS Mycoplasma genitalium.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=2097;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 33530 / G-37;
RX MEDLINE=96026346; PubMed=7569993;
RA Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A.,
RA Fleischmann R.D., Bult C.J., Kerlavage A.R., Sutton G., Kelley J.M.,
RA Fritchman J.L., Weidman J.F., Small K.V., Sandusky M., Fuhrmann J.L.,
RA Nguyen D.T., Uterback T.R., Saudek D.M., Phillips C.A., Merrick J.M.,
RA Tomb J.-F., Dougherty B.A., Bost K.F., Hu P.-C., Lucier T.S.,
RA Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.;
RT "The minimal gene complement of Mycoplasma genitalium.";
RL Science 270:397-403(1995).
CC -1- FUNCTION: THE RUVA-RUVB COMPLEX IN THE PRESENCE OF ATP RENATURES
CC CRUCIFORM STRUCTURE IN SUPERCOILED DNA WITH PALINDROMIC SEQUENCE,
CC INDICATING THAT IT MAY PROMOTE STRAND EXCHANGE REACTIONS IN
CC HOMOLOGOUS RECOMBINATION. RUVAB IS AN HELICASE THAT MEDIATES THE
CC HOLLIDAY JUNCTION MIGRATION BY LOCALIZED DENATURATION AND
CC REANNEALING (BY SIMILARITY).
CC -1- SUBUNIT: FORMS A COMPLEX WITH RUVA.
CC -1- SIMILARITY: BELONGS TO THE RUVB FAMILY.
CC -----
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CC -----
CC EMBL; U39717; AAC71584.1; -.
CC PIR; G64239; G64239.
CC TIGR; MG359; -.
CC HAMAP; MF 00016; -. 1.
CC InterPro; IPR003593; AAA_ATPase.
CC InterPro; IPR003959; AAA_ATPase_cent.
CC InterPro; IPR004605; RuvB.
CC Pfam; PF00004; AAA; 1.
CC SMART; SM00382; AAA; 1.
CC TIGRFAMs; TIGR00635; ruvb; 1.
CC DNA repair; SOS response; ATP-binding; DNA recombination; Helicase;
KW Complete proteome.
FT NP_BIND 45 52 ATP (POTENTIAL).
SQ SEQUENCE 307 AA; 35000 MW; 376E5138279E396C CRC64;

Query Match 86.7%; Score 26; DB 1; Length 307;
Best Local Similarity 66.7%; Pred. No. 83;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVEY 6
DB 241 SVDVQY 246

RESULT 25
RUVB_MYCPN STANDARD; PRT; 307 AA.
AC P75242;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Holliday junction DNA helicase ruvb.
GN RUVB OR MPN536 OR MP306.
OS Mycoplasma pneumoniae.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=2104;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 29342 / M129;
RX MEDLINE=97105885; PubMed=8948633;
RA Himmelfreich R., Hilbert H., Plagens H., Pirkl E., Li B.-C.,
RA Herrmann R.;
RT "Complete sequence analysis of the genome of the bacterium Mycoplasma
RT pneumoniae.";
RL Nucleic Acids Res. 24:4420-4449(1996).
CC -1- FUNCTION: THE RUVA-RUVB COMPLEX IN THE PRESENCE OF ATP RENATURES
CC CRUCIFORM STRUCTURE IN SUPERCOILED DNA WITH PALINDROMIC SEQUENCE,
CC INDICATING THAT IT MAY PROMOTE STRAND EXCHANGE REACTIONS IN
CC HOMOLOGOUS RECOMBINATION. RUVAB IS AN HELICASE THAT MEDIATES THE
CC HOLLIDAY JUNCTION MIGRATION BY LOCALIZED DENATURATION AND
CC REANNEALING (BY SIMILARITY).
CC -1- SUBUNIT: FORMS A COMPLEX WITH RUVA.
CC -1- SIMILARITY: BELONGS TO THE RUVB FAMILY.
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CC -----
CC EMBL; AB000028; AAB95954.1; -.
CC PIR; S73632; S73632.
CC HAMAP; MF 00016; -. 1.
CC InterPro; IPR003593; AAA_ATPase.
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DR InterPro; IPR003959; AAA_ATPase_centri.
DR InterPro; IPR004605; RuvB.
DR Pfam; PF00004; AAA; 1.
DR SMART; SM00382; AAA; 1.
DR TIGRfam; TIGR00635; ruvB; 1.
KW DNA repair; SOS response; ATP-binding; DNA recombination; Helicase;
KW Complete proteome.
FT NP BIND 45 52 ATP (POTENTIAL).
SQ SEQUENCE 307 AA; B1947D0C7AFFAF3A CRC64;

Query Match 86.7%; Score 26; DB 1; Length 307;
Best Local Similarity 66.7%; Pred. No. 83;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVEY 6
DB 241 SVDVQY 246

RESULT 26
FLIM_AGR75
ID _FLIM_AGR75 STANDARD; PRT; 321 AA.
AC (4457;
DT 15-DEC-1998 (Rel. 37, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Flagellar motor switch protein flim.
GN FLIM OR ATU0561 OR AGR_C_987.
OS Agrobacterium tumefaciens (strain C58 / ATCC 33970).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
OX NCBI_TaxID=176299;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97305159; PubMed=9161425;
RA Deakin W.J., Parker V.E., Loake G.J., Shaw C.H.;
RT "The Agrobacterium tumefaciens motor gene, motA, is in a linked
RT cluster with the flagellar switch protein genes, flig, flim and
RT flin";
RL Gene 189:139-141(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21608550; PubMed=11743193;
RA Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,
RA Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,
RA Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr.,
RA Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,
RA Kutayavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,
RA Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D.,
RA Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,
RA Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,
RA Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
RA Nester E.W.;
RT "The genome of the natural genetic engineer Agrobacterium tumefaciens
RT C58";
RL Science 294:2317-2323(2001).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=21608551; PubMed=11743194;
RA Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,
RA Quorillo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Wallin L.,
RA Houmiel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F.,
RA Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B.,
RA Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G.,
RA Cielo C., Slater S.;
RT "Genome sequence of the plant pathogen and biotechnology agent
RT Agrobacterium tumefaciens C58";
RL Science 294:2323-2328(2001).
CC -!- FUNCTION: FLIM IS ONE OF THREE PROTEINS (FLIG, FLIN, FLIM) THAT
CC FORM A SWITCH COMPLEX THAT IS PROPOSED TO BE LOCATED AT THE BASE
CC OF THE BASAL BODY. THIS COMPLEX INTERACTS WITH THE CHEY AND CHEZ
CC CHEMOTAXIS PROTEINS. IN ADDITION TO CONTACTING COMPONENTS OF THE
CC MOTOR THAT DETERMINE THE DIRECTION OF FLAGELLAR ROTATION (BY
CC

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CC SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Inner membrane-associated.
CC -!- SIMILARITY: BELONGS TO THE FLIM FAMILY.
CC
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CC or send an email to license@isb-sib.ch).
CC
DR EMBL; U63290; AAC45322.1; -.
DR EMBL; U95165; AAB71781.1; -.
DR EMBL; AE009025; AAL41578.1; ALT_INIT.
DR EMBL; AE007990; AAK86373.1; -.
DR FIR; D97427; D97427.
DR InterPro; IPR001543; SpoA.
DR Pfam; PF01052; SpoA; 1.
KW Chemotaxis; Flagella; Flagellar rotation; Inner membrane;
KW Complete proteome.
FT CONFLICT 157 157 G -> C (IN REF. 1).
FT CONFLICT 160 160 E -> V (IN REF. 1).
SQ SEQUENCE 321 AA; 34633 MW; D944CAE218C2D7B9 CRC64;

Query Match 86.7%; Score 26; DB 1; Length 321;
Best Local Similarity 66.7%; Pred. No. 87;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVEY 6
DB 60 AIDVEY 65

RESULT 27
VT2_MXVVL
ID _VT2_MXVVL STANDARD; PRT; 326 AA.
AC P29825;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Tumor necrosis factor soluble receptor precursor (Protein T2).
GN M092L OR T2.
OS Myxoma virus (strain Lausanne).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Leporipoxvirus.
OX NCBI_TaxID=311530;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91335768; PubMed=1651597;
RA Upton C., Macen J.L., Schreiber M., McFadden G.;
RT "Myxoma virus expresses a secreted protein with homology to the tumor
RT necrosis factor receptor gene family that contributes to viral
RT virulence";
RL Virology 184:370-382(1991).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20032073; PubMed=10562494;
RA Canonon C., Hota-Mitchell S., Chen L., Barrett J., Cao J.X.,
RA Macaulay C., Willer D., Evans D., McFadden G.;
RT "The complete DNA sequence of myxoma virus.";
RL Virology 264:298-318(1999).
CC -!- FUNCTION: BINDS TO TNF-ALPHA AND BETA. PROBABLY PREVENTS TNF TO
CC REACH CELLULAR TARGET AND THEREBY DEAMPENING THE POTENTIAL
CC ANTIVIRAL EFFECTS OF THE CYTOKINE.
CC -!- SIMILARITY: Contains 4 TNFR-Cys repeats.
CC
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CC EMBL; M95181; AAA46632.1; -.
CC DR EMBL; AF170726; AAL15046.1; -.
CC DR EMBL; AF170726; AAL14887.1; -.
CC DR EMBL; A23729; CAA01686.1; -.
CC DR PIR; A40566; GQVZML.
CC DR HSSP; P19438; INCF.
CC DR InterPro; IPR001368; TNFR_c6.
CC DR Pfam; PF00020; TNFR_c6; 2.
CC DR SMART; SM00208; TNFR; 3.
CC DR PROSITE; PS00652; TNFR_NGFR_1; 2.
CC DR PROSITE; PS00050; TNFR_NGFR_2; 2.
CC KW Receptor; Glycoprotein; Repeat; Signal.
CC FT SIGNAL 1 16
CC FT CHAIN 17 326
CC FT REPEAT 27 62
CC FT REPEAT 63 104
CC FT REPEAT 105 147
CC FT REPEAT 148 186
CC FT DISULFID 28 39
CC FT DISULFID 40 53
CC FT DISULFID 43 61
CC FT DISULFID 64 79
CC FT DISULFID 82 96
CC FT DISULFID 86 104
CC FT DISULFID 106 120
CC FT DISULFID 123 146
CC FT DISULFID 129 149
CC FT DISULFID 164 185
CC FT CARBOHYD 66 66
CC FT CARBOHYD 181 181
CC FT CARBOHYD 205 205
CC FT CARBOHYD 238 238
CC SQ SEQUENCE 326 AA; 35208 MW; ABB027E947292FF CRC64;

Query Match 86.7%; Score 26; DB 1; Length 326;
Best Local Similarity 66.7%; Pred. No. 89;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVEY 6
Db 287 NVDIEY 292

RESULT 28
RECA_LACLA
ID RECA_LACLA STANDARD; PRT; 341 AA.
AC Q59456;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE ReCA protein, plasmid (Recombinase A) (recALP).
GN RECAL.
OS Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
OG Plasmid pNP40.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
OX NCBI_TaxID=1360;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=DRC3;
RC MEDLINE=97251810; PubMed=9097419;
RA Garvey P., Rince A., Hill C., Fitzgerald G.F.;
RT "Identification of a reCA homolog (recALP) on the conjugative
RT lactococcal phage resistance plasmid pNP40: evidence of a role for
RT chromosomally encoded recAL in abortive infection.";
RL Appl. Environ. Microbiol. 63:1244-1251(1997).
CC -1- FUNCTION: CAN CATALYZE THE HYDOLYSIS OF ATP IN THE PRESENCE OF
CC SINGLE-STRANDED DNA, THE ATP-DEPENDENT UPTAKE OF SINGLE-STRANDED
CC DNA BY DUPLEX DNA, AND THE ATP-DEPENDENT HYBRIDIZATION OF
CC HOMOLOGOUS SINGLE-STRANDED DNAs. IT INTERACTS WITH LEXA CAUSING
CC ITS ACTIVATION AND LEADING TO ITS AUTOCATALYTIC CLEAVAGE.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).

-1- SIMILARITY: Belongs to the recA family.
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CC or send an email to license@isb-sib.ch)
CC EMBL; U36837; AAB52384.1; -.
CC DR HSSP; P03017; 2REB.
CC DR HAMAP; MF_00268; -.
CC DR InterPro; IPR003593; AAA_Atpase.
CC DR InterPro; IPR001553; RecA.
CC DR Pfam; PF00154; recA; 1.
CC DR PRINTS; PR00142; RECA.
CC DR ProDom; PD000229; RecA; 1.
CC DR SMART; SM00382; AAA; 1.
CC DR PROSITE; PS00321; RECA_1; 1.
CC DR PROSITE; PS00162; RECA_2; 1.
CC DR PROSITE; PS00163; RECA_3; 1.
CC KW Plasmid; DNA damage; DNA recombination; SOS response; ATP-binding;
CC DNA-binding.
CC FT NP_BIND 80 87
CC FT NP_BIND 87 87
CC SQ SEQUENCE 341 AA; 37177 MW; F9D4BCCEA69EAB5 CRC64;

Query Match 86.7%; Score 26; DB 1; Length 341;
Best Local Similarity 66.7%; Pred. No. 93;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVEY 6
Db 112 SLDIEY 117

RESULT 29
FIBG_RAT
ID FIBG_RAT STANDARD; PRT; 445 AA.
AC P02680;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-PEB-1996 (Rel. 33, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Fibrinogen gamma chain precursor.
GN FGG.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83129318; PubMed=6897622;
RA Crabtree G.R., Kant J.A.;
RT "Organization of the rat gamma-fibrinogen gene: alternative mRNA
RT splice patterns produce the gamma A and gamma B (gamma ) chains of
RT fibrinogen.";
RL Cell 31:159-166(1982).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=87174801; PubMed=3562236;
RA Morgan J.G., Holbrook N.J., Crabtree G.R.;
RT "Nucleotide sequence of the gamma chain gene of rat fibrinogen:
RT conserved intronic sequences.";
RN Nucleic Acids Res. 15:2774-2776(1987).
RN [3]
RP SEQUENCE OF 1-102 FROM N.A.
RX MEDLINE=84194000; PubMed=6232608;
RA Fowlkes D.M., Mullis N.T., Comeau C.M., Crabtree G.R.;
RT "Potential basis for regulation of the coordinately expressed
RT fibrinogen genes: homology in the 5' flanking regions.";
RL Proc. Natl. Acad. Sci. U.S.A. 81:2313-2316(1984).
CC -1- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET

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CC AGGREGATION.
CC -1- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -1- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms=2;
CC Name=Gamma-B;
CC IsoId=P02680-1; Sequence=Displayed;
CC Name=Gamma-A;
CC IsoId=P02680-2; Sequence=VSP 001538, VSP 001539;
CC MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT. THE SOFT CLOT IS
CC CONVERTED INTO THE HARD CLOT BY FACTOR XIII WHICH CATALYZES THE
CC EPSILON-(GAMMA-GLUTAMYL)LYSINE CROSS-LINKING BETWEEN GAMMA CHAINS
CC (STRONGER) AND BETWEEN ALPHA CHAINS (WEAKER) OF DIFFERENT
CC MONOMERS.
CC -1- SIMILARITY: Contains 1 fibrinogen C-terminal domain.
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CC or send an email to license@isb-sib.ch).
CC EMBL; J00733; ; NOT_ANNOTATED_CDS.
CC EMBL; J00734; ; NOT_ANNOTATED_CDS.
CC EMBL; J00735; ; NOT_ANNOTATED_CDS.
CC EMBL; X05860; CAA329289.1; -.
CC EMBL; X05861; CAA329289.1; JOINED.
CC EMBL; K01337; AAA98626.1; -.
CC PIR; A90828; FQRTGA.
CC HSSP; P02679; IFID.
CC InterPro; IPR002181; Fibrinogen_C.
CC Pfam; PF00147; fibrinogen_C; 1.
CC SMART; SM00186; FBG; 1.
CC PROSITE; PS00514; FIBRIN AG C DOMAIN; 1.
CC Blood coagulation; Glycoprotein; Calcium; Platelet; Plasma;
CC Alternative splicing; Signal.
CC SIGNAL 1 25
CC CHAIN 26 445
CC DISULFID 34 34
CC DISULFID 35 35
CC DISULFID 45 45
CC DISULFID 49 49
CC DISULFID 161 161
CC DISULFID 165 165
CC DISULFID 179 208
CC DISULFID 352 365
CC VARSPPLIC 435 437
CC VARSPPLIC 438 445
CC CONFLICT 296 296
CC SEQUENCE 445 AA; 50632 MW; 9D61CC0C168B17A9 CRC64;
Query Match 86.7%; Score 26; DB 1; Length 445;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 VDVEY 6
DB 440 VDVEY 444
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RESULT 30
SYG MYCTU
ID_ SYG MYCTU STANDARD; PRT; 463 AA.
AC O6532;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE GLYCYL-tRNA synthetase (EC 6.1.1.14) (Glycine--tRNA ligase) (GlyRS).
DE GLYS OR RV2357C OR MT2426 OR MTCV27.23 OR MTCV98.26.
GN Mycobacterium tuberculosis.
OS Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H37RV;
RX MEDLINE=98295987; PubMed=9634230;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
RA Gordon S.V., Eigmeier K., Gas S., Barry C.E. III, Tekaita F.,
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy J.,
RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
RA Sulston J.E., Taylor K., Whitehead S., Barrett B.G.;
RA "Deciphering the biology of Mycobacterium tuberculosis from the
RT complete genome sequence.";
RT Nature 393:537-544 (1998).
RL [2]
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CDC 1551 / Oshkosh;
RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
RA Peterson J., Deboy R., Dodson R., Gwinn M.B., Haft D., Hickey E.,
RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
RA Bishai W.;
RA "Whole genome comparison of Mycobacterium tuberculosis clinical and
RT laboratory strains.";
RT Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
RL -1- CATALYTIC ACTIVITY: ATP + glycine + tRNA(Gly) = AMP + diphosphate
CC + glycyL-tRNA(Gly).
CC -1- SUBUNIT: Homodimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: Belongs to class-II aminoacyl-tRNA synthetase family.
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CC EMBL; Z95208; CAB08466.1; -.
CC EMBL; AB007082; AAK46720.1; -.
CC PIR; D70585; D70585.
CC HSSP; P56206; LATI.
CC TIGR; MT2426; -.
CC TubercuList; Rv2357c; -.
CC HAMAP; MF_00253; -.
CC InterPro; IPR004154; HGTP_anticonodon.
CC InterPro; IPR002314; tRNA-synt_2b.
CC InterPro; IPR002315; tRNA-synt_gly.
CC InterPro; IPR006195; tRNA_ligase_II.
CC Pfam; PF03129; HGTP_anticonodon; 1.
CC Pfam; PF00587; tRNA-synt_2b; 1.
CC PRINTS; PR01043; TRNASYNTHGLY.
CC TIGRFAMs; TIGR00389; glyS_dimeric; 1.
CC PROSITE; PS50862; AA tRNA_LIGASE II; 1.
CC Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
CC Complete proteome.
CC SEQUENCE 463 AA; 52937 MW; E8BDCE20B65538F7 CRC64;
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Query Match      86.7%; Score 26; DB 1; Length 463;
Best Local Similarity 66.7%; Pred. No. 1.3e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 SVDVEY 6
DB      268 TVDIEY 273
      :|||:

RESULT 31
COBQ_PYRFU      STANDARD;      PRT;      483 AA.
AC      Q8U328;
DT      28-FEB-2003 (Rel. 41, Created)
DT      28-FEB-2003 (Rel. 41, Last sequence update)
DT      28-FEB-2003 (Rel. 41, Last annotation update)
DE      Probable cobyrlic acid synthase.
GN      COBQ OR PF0301.
OS      Pyrococcus furiosus.
OC      Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC      Pyrococcus.
OX      NCBI_TaxID=2261;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=Vc1 / DSM 3638 / ATCC 43587 / JCM 8422;
RA      Weiss R.B., Dunn D.M., Robb F.T., Brown J.R.;
RT      "The complete sequence of the Pyrococcus furiosus genome."
RL      Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
CC      -!- FUNCTION: Catalyzes amidations at positions B, D, E, and G on
CC      adenosylcobyrinic A,C-diamide. NH(2) groups are provided by
CC      glutamine, and one molecule of ATP is hydrolyzed for each
CC      amidation (By similarity).
CC      -!- PATHWAY: Cobalamin biosynthesis.
CC      -!- SIMILARITY: BELONGS TO THE COBB/COBQ FAMILY. COBQ SUBFAMILY.
CC
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CC
DR      EMBL; AE010154; AAL80425.1; -
DR      HAMAP; MF 00028; -; 1.
DR      InterPro; IPR002586; CbiA_P.
DR      InterPro; IPR004459; CobQ.
DR      Pfam; PF01656; CbiA; 1.
DR      TIGRFAMs; TIGR00313; cobQ; 1.
KW      Cobalamin biosynthesis; Complete proteome.
SQ      SEQUENCE 483 AA; 54538 MW; 277915AE1B35D726 CRC64;

Query Match      86.7%; Score 26; DB 1; Length 483;
Best Local Similarity 66.7%; Pred. No. 1.3e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 SVDVEY 6
DB      471 SIDVDY 476
      :|||:

RESULT 32
ARAA_THEME      STANDARD;      PRT;      496 AA.
AC      Q9WYB3;
DT      28-FEB-2003 (Rel. 41, Created)
DT      28-FEB-2003 (Rel. 41, Last sequence update)
DT      28-FEB-2003 (Rel. 41, Last annotation update)
DE      L-arabinose isomerase (EC 5.3.1.4).
GN      ARAA OR TM0276.
OS      Thermotoga maritima.
OC      Bacteria; Thermotogae; Thermotogales; Thermotogaceae; Thermotoga.
OX      NCBI_TaxID=2336;

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[1]
RN      SEQUENCE FROM N.A.
RP      STRAIN=MSB8 / DSM 3109;
RC      MEDLINE=99287316; PubMed=10360571;
RA      Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
RA      Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
RA      McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett K.M.,
RA      Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
RA      Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
RA      Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
RT      "Evidence for lateral gene transfer between Archaea and Bacteria from
RT      genome sequence of Thermotoga maritima."
RL      Nature 399:323-329(1999).
CC      -!- CATALYTIC ACTIVITY: L-arabinose = L-ribulose.
CC      -!- PATHWAY: L-arabinose catabolism; first step.
CC      -!- SIMILARITY: Belongs to the arabinose isomerase family.
CC
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CC
DR      EMBL; AE001709; AAD35365.1; -
DR      PIR; B72398; B72398.
DR      TIGR; TM0276; -; 1.
DR      HAMAP; MF 00519; -; 1.
DR      InterPro; IPR003762; Lara_isomerase.
DR      Pfam; PF02610; Arabinose Isome; 1.
DR      ProDom; PD018364; Lara_isomerase; 1.
KW      Isomerase; Arabinose catabolism; Complete proteome.
SQ      SEQUENCE 496 AA; 56658 MW; D6AA88752A183DE0 CRC64;

Query Match      86.7%; Score 26; DB 1; Length 496;
Best Local Similarity 66.7%; Pred. No. 1.4e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 SVDVEY 6
DB      451 AIDVEY 456
      :|||:

RESULT 33
SYK_CHLTR      STANDARD;      PRT;      526 AA.
AC      Q84786;
DT      30-MAY-2000 (Rel. 39, Created)
DT      30-MAY-2000 (Rel. 39, Last sequence update)
DT      28-FEB-2003 (Rel. 41, Last annotation update)
DE      Lysyl-tRNA synthetase (EC 6.1.1.6) (Lysine--tRNA ligase) (LysRS).
GN      LYSS OR CT781.
OS      Chlamydia trachomatis.
OC      Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
OX      NCBI_TaxID=813;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=D/UW-3/Cx;
RX      MEDLINE=9900809; PubMed=9784136;
RA      Stephens R.S., Kalman S., Lammel C.J., Fan J., Marathe R., Aravind L.,
RA      Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V.,
RA      Davis R.W.;
RT      "Genome sequence of an obligate intracellular pathogen of humans:
RT      Chlamydia trachomatis."
RL      Science 282:754-759(1998).
CC      -!- CATALYTIC ACTIVITY: ATP + L-lysine + tRNA(Lys) = AMP + diphosphate
CC      + L-lysyl-tRNA(Lys).
CC      -!- COFACTOR: Binds 3 magnesium ions per subunit (By similarity).
CC      -!- SUBUNIT: Homodimer (By similarity).
CC      -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC      -!- SIMILARITY: Belongs to class-II aminoacyl-tRNA synthetase family.
CC

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CC EMBL: AE001350; AAC68376.1; --  
 CC PIR: E71472; E71472.  
 CC HSP: P14825; I510.  
 CC HAMAP: MF\_00252; -, 1.  
 CC InterPro: IPR004364; tRNA-synt\_2.  
 CC InterPro: IPR002313; tRNA-syntlys\_2.  
 CC InterPro: IPR004365; tRNA anti-  
 CC InterPro: IPR006195; tRNA\_ligase\_II.  
 CC Pfam: PF00152; tRNA-synt\_2; 1.  
 CC Pfam: PF01336; tRNA anti; 1.  
 CC PRINTS: PR00982; TRNASYNTHLYS.  
 CC TIGRFAMs: TIGR00499; lysS bact; 1.  
 CC PROSITE: PS50862; AA tRNA LIGASE II; 1.  
 CC Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;  
 CC Metal-binding; Magnesium; Complete proteome.  
 CC METAL 431 MAGNESIUM 1 (BY SIMILARITY).  
 CC METAL 438 438 MAGNESIUM 1 AND 2 (BY SIMILARITY).  
 CC SEQUENCE 526 AA; 60106 MW; BEAE8A47DDDD041C CRC64;

Query Match 86.7%; Score 26; DB 1; Length 526;  
 Best Local Similarity 83.3%; Pred. No. 1.5e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVEY 6  
 DB 2 SVEVEY 7

RESULT 34  
 UVR\_C MYCBV STANDARD; PRT; 571 AA.  
 AC 084856;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE UvrABC system protein C (UvrC protein) (Excinuclease ABC subunit C).  
 GN UVR\_C  
 OS Mycoplasma bovis.  
 OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.  
 OX NCBI\_TaxID=28903;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=PG45;  
 RX MEDLINE=98329280; PubMed=9664578;  
 RA Subramaniam S., Bergonier D., Fournier F., Capaul S., Schlatter Y.,  
 RA Nicolet J., Frey J.;  
 RT "Species identification of Mycoplasma bovis and Mycoplasma agalactiae  
 RT based on the uvrC genes by PCR";  
 RL Mol. Cell. Probes 12:161-169(1998).  
 CC -!- FUNCTION: The UvrABC repair system catalyzes the recognition and  
 CC processing of DNA lesions. UvrC both incises the 5' and 3' sides  
 CC of the lesion. The N-terminal half is responsible for the 3'  
 CC incision and the C-terminal half is responsible for the 5'  
 CC incision (By similarity).  
 CC -!- SUBUNIT: Interacts with uvrB in an incision complex (By  
 CC similarity).  
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).  
 CC -!- SIMILARITY: Belongs to the uvrC family.  
 CC -!- SIMILARITY: Contains 1 UVR domain.

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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC EMBL: AF003959; AAC32309.1; --  
 CC HAMAP: MF\_00203; -, 1.  
 CC InterPro: IPR003583; HHH 1.  
 CC InterPro: IPR001943; UvrB/C.  
 CC InterPro: IPR004791; UvrC.  
 CC InterPro: IPR001162; UvrC C.  
 CC InterPro: IPR000305; UvrC\_N.  
 CC Pfam: PF01541; Exci\_endo\_N; 1.  
 CC Pfam: PF02151; UVR; 1.  
 CC ProDom: PD005870; UvrC\_C; 1.  
 CC SMART: SM00465; GIYC; 1.  
 CC SMART: SM00278; HbH1; 1.  
 CC TIGRFAMs: TIGR00194; uvrC; 1.  
 CC PROSITE: PS50151; UVR; 1.  
 CC PROSITE: PS50164; UVR\_C\_1; 1.  
 CC PROSITE: PS50165; UVR\_C\_2; 1.  
 CC SOS response; Excision nuclease; DNA repair; DNA recombination;  
 CC DNA excision.  
 CC DOMAIN 184 219 UVR.  
 CC SEQUENCE 571 AA; 66463 MW; 717DA202CA50DCE3 CRC64;

Query Match 86.7%; Score 26; DB 1; Length 571;  
 Best Local Similarity 83.3%; Pred. No. 1.6e+02;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SVDVEY 6  
 DB 409 SADVEY 414

RESULT 35  
 ACE\_HABIE STANDARD; PRT; 611 AA.  
 AC Q10715;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Angiotensin-converting enzyme precursor (EC 3.4.15.1) (Dipeptidyl  
 DE carboxypeptidase I) (Kininase II).  
 GN ACE.  
 OS Haemaphysalis irritans exigua (Buffalo fly).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Muscoidea;  
 OC Muscidae; Haematobia.  
 OX NCBI\_TaxID=34678;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=96215437; PubMed=8647080;  
 RA Wiljffels G.L., Fitzgerald C., Gough J., Riding G.A., Elvin C.,  
 RA Kemp D.J., Willadsen P.;  
 RT "Cloning and characterisation of angiotensin-converting enzyme from  
 RT the dipteran species, Haematobia irritans exigua, and its expression  
 RL in the maturing male reproductive system";  
 RL Eur. J. Biochem. 237:414-423(1996).  
 CC -!- FUNCTION: INVOLVED IN THE SPECIFIC MATURATION OR DEGRADATION OF A  
 CC NUMBER OF BIOACTIVE PEPTIDES.  
 CC -!- CATALYTIC ACTIVITY: Release of a C-terminal dipeptide,  
 CC oligopeptide-|-Xaa-Xbb, when Xaa is not Pro, and Xbb is neither  
 CC Asp nor Glu. Converts angiotensin I to angiotensin II.  
 CC -!- COFACTOR: Binds 1 zinc ion (By similarity).  
 CC -!- TISSUE SPECIFICITY: EXPRESSED IN THE COMPOUND GANGLION AND IN THE  
 CC POSTERIOR REGION OF THE MIDGUT.  
 CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M2.

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CC CC EMBL: L43965; AAA70427.1; -.
DR DR PIR: S65472; S65472.
DR DR MEROPS; M02.003; -.
DR DR InterPro; IPR001545; Peptidase M2.
DR DR InterPro; IPR006025; Zn_MTPeptidase.
DR DR Pfam; PF01401; Peptidase M2; 1.
DR DR PRINTS; PR00791; Peptidase M2; 1.
DR DR ProDom; PD004184; Peptidase M2; 1.
DR DR PROSITE; PS00142; ZINC_PROTEASE; 1.
DR DR Hydrolase; Metalloprotease; Carboxypeptidase; Zinc; Dipeptidase;
KW Glycoprotein; Signal.
FT SIGNAL 1 17
FT CHAIN 18 611
FT METAL 367 367
FT ACT_SITE 368 368
FT METAL 371 371
FT CARBOHYD 53 53
FT CARBOHYD 196 196
FT CARBOHYD 531 531
SQ SEQUENCE 611 AA; 70505 MW; A43D6DF5A83ECB53 CRC64;

Query Match 86.7%; Score 26; DB 1; Length 611;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SVDVEY 6
Db 499 SADVEY 504

RESULT 36
ACE_DROME
ID ACE_DROME STANDARD; PRT; 615 AA.
AC Q10714; Q27572; Q9NKE4; Q9TX66; Q9JUV3;
DT 01-NOV-1997 (Rel. 35, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Angiotensin-converting enzyme precursor (EC 3.4.15.1) (Dipeptidyl
carboxypeptidase 1) (kininase 1).
GN ANCE OR RACE OR BG:DS08220.3 OR CG8827.
OS Drosophila melanogaster (fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RN SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=94040210; PubMed=8224398;
RA Cornell M.J., Coates D., Isaac R.E.;
RT "Characterisation of putative Drosophila angiotensin converting enzyme
cDNA clones.";
RL Biochem. Soc. Trans. 21:243-243(1993).
RN [2]
RN SEQUENCE FROM N.A.
RX MEDLINE=95293950; PubMed=7775412;
RA Cornell M.J., Williams T.A., Lamango N.S., Coates D., Corvol P.,
RA Soubrier F., Hoheisel J., Lehrach H., Isaac R.E.;
RT "Cloning and expression of an evolutionary conserved single-domain
angiotensin converting enzyme from Drosophila melanogaster.";
RL J. Biol. Chem. 270:13613-13619(1995).
RN [3]
RN REVISIONS.
RA Cornell M.J.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
RN [4]
RN SEQUENCE FROM N.A.
RC STRAIN=Canton-S;
RX MEDLINE=96028519; PubMed=7547464;
RA Tatei K., Cai H., Ip Y.T., Levine M.;
RT "Race: a Drosophila homologue of the angiotensin converting enzyme.";
RN [5]
RN MECH. Dev. 51:157-168(1995).
RL [5]
RN SEQUENCE FROM N.A.
RC STRAIN=Berkley;
RX MEDLINE=99403001; PubMed=10471707;
RA Ashburner M., Misra S., Rote J., Lewis S.E., Blazej R.G., Davis T.,
RA Doyle C., Galle R.F., George R.A., Harris N.L., Hartzell G.,
RA Harvey D., Hong L., Houston K.A., Hoskins R.A., Johnson G.,
RA Martin C.H., Moshrefi A., Palazzolo M., Reese M.G., Spradling A.C.,
RA Tsang G., Wan K.H., Whitelaw K., Celnik S.E., Rubin G.M.;
RT "An exploration of the sequence of a 2.9-Mb region of the genome of
Drosophila melanogaster: the Adh region.";
RN Genetics 153:179-219(1999).
RN [6]
RN SEQUENCE FROM N.A.
RC STRAIN=Berkley;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Bottner P.,
RA Chertis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Hestis N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai X.,
RA Laoko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Matti B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy J., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Furi V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirska R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
RN [7]
RN SEQUENCE FROM N.A.
RC STRAIN=Embryo;
RX MEDLINE=22426066; PubMed=12537569;
RA Stapleton M., Carlson J.W., Brokstein P., Yu C., Champe M.,
RA George R.A., Guarin H., Krommiller B., Pacleb J.M., Park S., Wan K.H.,
RA Rubin G.M., Celnik S.E.;
RT "A Drosophila full-length cDNA resource.";
RL Genome Biol. 3:RESEARCH0080.1-RESEARCH0080.8(2002).
RN [8]
RN FUNCTION: MAY PLAY A ROLE IN THE CONTRACTIONS OF THE HEART, GUT
AND TESTES.
CC -1- CATALYTIC ACTIVITY: Release of a C-terminal dipeptide,
CC oligopeptide-|-Xaa-Xbb, when Xaa is not Pro, and Xbb is neither
CC Asp nor Glu. Converts angiotensin I to angiotensin II.
CC -1- COFACTOR: Binds 1 zinc ion (By similarity).
CC -1- SUBCELLULAR LOCATION: Extracellular.
CC -1- DEVELOPMENTAL STAGE: EXPRESSED IN THE AMNIOEROSA DURING GERM BAND
CC ELONGATION, SHORTENED AND HEART MORPHOGENESIS. EXPRESSED IN

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CC MIDGUT THROUGHOUT EMBRYOGENESIS.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M2.
CC -----
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CC -----
DR ENBL; U25344; AAB02171.1; -
DR ENBL; U34599; AAC46902.1; -
DR ENBL; AE003408; AAF44834.1; -
DR ENBL; AE003641; AAF53353.2; -
DR ENBL; AY061129; AAL28677.1; -
DR MEROPS; M02.003; -
DR FlyBase; FBgn0012037; Ance.
DR GO; GO:0004246; F:peptidyl-di-peptidase A activity; IDA.
DR InterPro; IPR001548; Peptidase_M2.
DR InterPro; IPR006025; Zn_MTPeptidase.
DR Pfam; PF01401; Peptidase_M2; 1.
DR PRINTS; PR00791; PEPDIPPTASEA.
DR PRODOM; PD004184; Peptidase_M2; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; 1.
DR Hydrolase; Metalloprotease; Carboxypeptidase; Zinc; Dipeptidase;
KW Glycoprotein; Signal.
FT SIGNAL 17 POTENTIAL.
FT CHAIN 18 615 ANGIOTENSIN-CONVERTING ENZYME.
FT METAL 367 367 ZINC (CATALYTIC) (BY SIMILARITY).
FT ACT SITE 368 368 BY SIMILARITY.
FT METAL 371 371 ZINC (CATALYTIC) (BY SIMILARITY).
FT CARBOHYD 53 53 N-LINKED (GLNAC. .) (POTENTIAL).
FT CARBOHYD 196 196 N-LINKED (GLNAC. .) (POTENTIAL).
FT CARBOHYD 311 311 N-LINKED (GLNAC. .) (POTENTIAL).
FT CONFLICT 48 51 WAYS -> GPMR (IN REF. 4).
FT CONFLICT 141 141 C -> S (IN REF. 4).
FT CONFLICT 293 293 G -> A (IN REF. 3).
FT CONFLICT 346 346 I -> T (IN REF. 5, 6 AND 7).
FT CONFLICT 365 365 V -> E (IN REF. 1).
FT CONFLICT 402 402 S -> A (IN REF. 1).
FT CONFLICT 414 414 I -> T (IN REF. 1).
FT CONFLICT 486 486 S -> T (IN REF. 4).
FT CONFLICT 533 533 V -> M (IN REF. 4).
FT CONFLICT 547 547 A -> R (IN REF. 3).
SQ SEQUENCE 615 AA; 70926 MW; 9E3F9A41C51B9485 CRC64;

Query Match 86.7%; Score 26; DB 1; Length 615;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SVDVEY 6
Db 499 SADVEY 504

RESULT 37
RAPI SCHPO
ID RAPI SCHPO STANDARD; PRT; 693 AA.
AC Q96TL7; Q9UTW1; Q9UUI5;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE DNA-binding protein rap1.
GN RAPI OR SPBC1778.02.
OS Schizosaccharomyces pombe (fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCB1_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A., FUNCTION, SUBUNIT, AND SUBCELLULAR LOCATION.
RX MEDLINE=21534324; PubMed=11676924;

```

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RA Chikashige Y., Hiraoka Y.;
RT "Telomere binding of the Rap1 protein is required for meiosis in
RT fission yeast.";
RL Curr. Biol. 11:1618-1623(2001).
RN [2]
RP SEQUENCE FROM N.A., FUNCTION, AND SUBUNIT.
RX MEDLINE=21534325; PubMed=11676925;
RA Kanoh J., Ishikawa F.;
RT "Rap1 and spRif1, recruited to telomeres by Taz1, are essential for
RT telomere function in fission yeast.";
RL Curr. Biol. 11:1624-1630(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=21848401; PubMed=11859360;
RA Wood V., Gwilliam R., Rajandream K.A., Lyne M., Lyne R., Stewart A.,
RA Sgouras J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymoprez B.,
RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Motier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gallardet C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Cerrutini L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
RT "The genome sequence of Schizosaccharomyces pombe.";
RL Nature 415:871-880(2002).
RN [4]
RP SEQUENCE OF 164-312 FROM N.A.
RC STRAIN=968 h90;
RX MEDLINE=20223869; PubMed=10759889;
RA Ding D.-Q., Tomita Y., Yamamoto A., Chikashige Y., Haraguchi T.,
RA Hiraoka Y.;
RT "Large-scale screening of intracellular protein localization in living
RT fission yeast cells by the use of a GFP-fusion genomic DNA library.";
RL Genes Cells 5:169-190(2000).
CC -1- FUNCTION: Involved in the regulation of telomere length,
CC clustering and has a specific role in telomere position effect
CC (TPE). Unlike yeast, exhibits now effect in transcription
CC regulation.
CC -1- SUBUNIT: Interacts with taz1. Unlike yeast does not interact with
CC rif1.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- SIMILARITY: Contains 1 BRCT domain.
CC -----
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CC -----
DR ENBL; AB061738; BAB70735.1; -
DR ENBL; AY034032; AAK57740.1; -
DR ENBL; AL049489; CAC39280.1; -
DR ENBL; AB027870; BAA87174.1; -
DR ENBL; AB027983; BAA87267.1; -
DR GeneDB_Spombe; SPBC1778.02; -

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DR InterPro; IPR001357; BRCT.
DR PROSITE; PS0172; BRCT; 1.
KW DNA-binding; Telomere; Nuclear protein.
FT DOMAIN 81 105 BRCT.
SQ SEQUENCE 693 AA; 79526 MW; 77C5070697D1A9CF CRC64;

Query Match      86.7%; Score 26; DB 1; Length 693;
Best Local Similarity 66.7%; Pred. No. 2e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVEY 6
DB 249 SIDVDY 254

RESULT 38
YPRF_BACSU STANDARD; PRT; 749 AA.
AC PS0830;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Putative helicase yprA.
GN YPRF.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
CX NCBI_TaxID=1423;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=168 / Marburg;
RX MEDLINE=96349105; PubMed=8760912;
RA Sorokin A.V., Azevedo V., Zumbstein E., Galleron N., Ehrlich S.D.,
RA Serror P.;
RT "Sequence analysis of the Bacillus subtilis chromosome region between
RT the serA and kds loci cloned in a yeast artificial chromosome.";
RL Microbiology 142:2005-2016(1996).
RN [2]
SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=98044033; PubMed=9384377;
RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borcherdt S.,
RA Borriess R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Denizot P., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,
RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Chim S.Y., Glaser P., Goffeau A., Gollightly E.J., Grandi G.,
RA Guiseppe G., Guy B.J., Haga K., Haele J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Joris B., Karamata D., Kasahara Y., Klaer-Blanchard M., Klein C.,
RA Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Lee S.M., Levine A., Liu H., Masuda S., Maue C., Medigue C.,
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Presecan E., Pujić C., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadate Y.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA Sekiguchi J., Sekowska H., Seror S.J., Serror P., Shin B.S., Soldo B.,
RA Sorokin A., Taccioni E., Takagi T., Takahashi H., Takenaru K.,
RA Takeuchi M., Tanakoshi A., Tanaka T., Terpsira P., Tognoni A.,
RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
RA Viari A., Wambutt R., Wedler E., Wedler H., Weitzenecker T.,
RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
RA Yoshida K., Yoshikawa H.F., Zumbstein E., Yoshikawa H., Danchin A.;
RT "The complete genome sequence of the Gram-positive bacterium Bacillus
RT subtilis.";
RL Nature 390:249-256(1997).
CC -1- SIMILARITY: BELONGS TO THE HELICASE FAMILY.

```

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EMBL; L47838; AAB38468.1; -.  
EMBL; Z99115; CAB14139.1; -.  
PIR; B69941; B69941.  
Subtilist; BG11451; YPRF.  
InterPro; IPR001410; DEAD.  
DR InterPro; IPR001650; Helicase\_C.  
DR Pfam; PF00270; DEAD; 1.  
DR Pfam; PF00271; helicase\_C; 1.  
DR SMART; SM00487; DEXDC; 1.  
DR SMART; SM00490; HELIC; 1.  
KW Hypothetical protein; Hydrolase; Helicase; ATP-binding;  
Complete proteome.  
FT NP\_BIND 76 83 ATP (BY SIMILARITY).  
FT SITE 185 188 DEVH BOX.  
FT SITE 185 188  
SQ SEQUENCE 749 AA; 84569 MW; 3F653EFA8EC3A7EE CRC64;

Query Match 86.7%; Score 26; DB 1; Length 749;  
Best Local Similarity 100.0%; Pred. No. 2.2e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDVVEY 6  
DB 554 VDVVEY 558

RESULT 39  
RPC2\_MOUSE STANDARD; PRT; 756 AA.  
AC P59470;  
DT 15-SEP-2003 (Rel. 42, Created)  
DT 15-SEP-2003 (Rel. 42, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE DNA-directed RNA polymerase III subunit 127.6 kDa polypeptide  
DE (EC 2.7.7.6) (RNA polymerase III subunit 2) (RPC2) (Fragments).  
GN POLR3B.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
RX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE OF 1-551 FROM N.A.  
RC STRAIN=CS7BL/6J; TISSUE=Spinal cord;  
RX MEDLINE=22354683; PubMed=12466851;  
RA Okazaki I., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,  
RA Nikaide I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,  
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,  
RA Balzarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,  
RA Schriml L.M., Kanapin A., Matsuda H.A., Batalov S., Beisel K.W.,  
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,  
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,  
RA Gaasterland T., Gariboldi M., Giasi C., Godzik A., Gough J.,  
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,  
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,  
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,  
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,  
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,  
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,  
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,  
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,  
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tonika M.,  
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,  
RA Wilming L.G., Wyshaw-Boris A., Yanagisawa M., Yang I., Yang L.,  
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayateu N.,  
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,  
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,

RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,  
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,  
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,  
RA Birney E., Hayashizaki Y.,  
RT "Analysis of the mouse transcriptome based on functional annotation of  
RL 60,770 full-length cDNAs." ;  
RL Nature 420:563-573 (2002). ;  
RN [2]  
RP SEQUENCE OF 552-756 FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Mammary gland;  
RX MEDLINE=22388257; PubMed=12477932;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klautner R.D., Collins F.S., Wagner L., Shenmen C.F., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Schetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Murry D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield V.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,  
RT "Generation and initial analysis of more than 15,000 full-length  
RT human and mouse cDNA sequences." ;  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
CC -!- FUNCTION: DNA-dependent RNA polymerase catalyzes the transcription  
CC of DNA into RNA using the four ribonucleoside triphosphates as  
CC substrates (By similarity).  
CC -!- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +  
CC {RNA}(N).  
CC -!- SUBUNIT: RNA polymerase III consists of about 15 different  
CC subunits. This subunit is the second largest component of RNA  
CC polymerase III (By similarity).  
CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).  
CC -!- SIMILARITY: Belongs to the RNA polymerase beta chain family.  
CC -----  
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CC -----  
DR EMBL; AK039366; BAC30327.1; -;  
DR EMBL; BC044796; AAH4796.1; -;  
KW Transferase; DNA-directed RNA polymerase; Transcription; Zinc;  
KW Zinc-finger; Nuclear protein. C4-TYPE (POTENTIAL).  
FT ZN FING 703 718  
FT NON\_CONS 551 552  
FT NON\_TER 756 756  
SQ SEQUENCE 756 AA; 85062 MW; 336763B7CEBBAFB8 CRC64;  
  
Query Match 86.7%; Score 26; DB 1; Length 756;  
Best Local Similarity 66.7%; Pred. No. 2.2e+02;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 SVDVEY 6  
Db 114 TVDIEY 119  
  
RESULT 40  
YLIE\_ECOLI  
ID YLIE\_ECOLI STANDARD; PRT; 782 AA.  
AC P75800;  
DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Hypothetical protein yliE.  
GN YLIE OR B0833.  
OS Escherichia coli.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Escherichia.  
OX NCBI\_TaxID=562;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=K12 / MG1655;  
RX MEDLINE=97426617; PubMed=9278503;  
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,  
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,  
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,  
RA Mau B., Shao Y.;  
RT "The complete genome sequence of Escherichia coli K-12." ;  
RL Science 277:1453-1474 (1997).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=K12;  
RX MEDLINE=97061202; PubMed=8905232;  
RA Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A.,  
RA Ikenoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,  
RA Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,  
RA Mori H., Motomura K., Nakamura Y., Nishimoto H., Nishio Y., Saito N.,  
RA Sasaki G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,  
RA Yano M., Horuchi T.;  
RT "A 718-kb DNA sequence of the Escherichia coli K-12 genome  
RT corresponding to the 12.7-28.0 min region on the linkage map." ;  
RL DNA Res. 3:137-155 (1996).  
CC -!- SIMILARITY: Contains 1 EAL domain.  
CC -----  
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CC -----  
DR EMBL; AE000185; AAC73920.1; -;  
DR EMBL; D90721; BAA35528.1; -;  
DR EMBL; D90722; BAA35536.1; -;  
DR PIR; A64821; A64821.  
DR EcoGene; EGI3476; yliE.  
DR InterPro; IPR001633; EAL.  
DR Pfam; PF00563; EAL; 1  
DR SMART; SM00052; DUF2; 1.  
DR PROSITE; PS50883; EAL; 1.  
KW Hypothetical protein; Complete proteome.  
FT DOMAIN 527 781  
SQ SEQUENCE 782 AA; 90048 MW; 508DFB068611DFB CRC64;  
  
Query Match 86.7%; Score 26; DB 1; Length 782;  
Best Local Similarity 83.3%; Pred. No. 2.3e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 SVDVEY 6  
Db 250 SVDPEY 255  
  
RESULT 41  
DPO2\_AERPE  
ID DPO2\_AERPE STANDARD; PRT; 784 AA.  
AC O93746;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE DNA polymerase II (EC 2.7.7.7).  
GN POLB OR APE2098.  
OS Aeropyrum pernix.



OC Archaea; Crenarchaeota; Thermoprotei; Desulfurococcales;  
 OC Desulfurococaceae; Aeropyrum.  
 OX NCBI\_TaxID=56636;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=KJ;  
 RA Iehino Y., Cann I.K.;  
 RT "Isolation of the genes encoding two alpha-like DNA polymerases from  
 RT Aeropyrum pernix.";  
 RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=KJ;  
 RA MEDLINE=99310339; PubMed=10382966;  
 RA Kawarabayashi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Y.,  
 RA Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankai A., Kosugi H.,  
 RA Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H.,  
 RA Takamaki M., Masuda S., Funahashi T., Tanaka T., Kudoh Y.,  
 RA Yamazaki J., Kishida N., Oguchi A., Aoki K.-I., Kubota K.,  
 RA Nakamura Y., Nomura N., Sako Y., Kikuchi H.;  
 RT "Complete genome sequence of an aerobic hyper-thermophilic  
 RT crenarchaeon, Aeropyrum pernix K1.";  
 RL DNA Res. 6:83-101(1999).  
 CC -!- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate  
 CC + {DNA}[N].  
 CC -!- SIMILARITY: BELONGS TO THE DNA POLYMERASE TYPE-B FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL; AB017501; BAA75663.1; -  
 DR EMBL; AP000063; BAB81109.1; -  
 DR PR; E72515; E72515.  
 DR HSP; P56689; ITGO.  
 DR InterPro; IPR006172; DNA\_pol\_B.  
 DR InterPro; IPR006134; DNA\_pol\_B\_dom.  
 DR InterPro; IPR006133; DNA\_pol\_B\_exo.  
 DR InterPro; IPR004578; PolX.  
 DR Pfam; PF00136; DNA\_pol\_B; 1.  
 DR Pfam; PF03104; DNA\_pol\_B\_exo; 1.  
 DR SMART; SM00486; POLEB; 1.  
 DR TIGRfams; TIGR00592; pol2; 1.  
 DR PROSITE; PS00116; DNA\_POLYMERASE\_B; 1.  
 KW Transferase; DNA-directed DNA polymerase; DNA replication;  
 KW DNA-binding; Complete proteome.  
 FT CONFLICT 104 104 E -> K (IN REF. 1).  
 FT CONFLICT 306 319 KIGERTVLEWQIG -> R (IN REF. 1).  
 FT CONFLICT 355 355 E -> Q (IN REF. 1).  
 FT CONFLICT 754 759 LRILQY -> SAHTSSN (IN REF. 1).  
 FT CONFLICT 763 763 T -> I (IN REF. 1).  
 SQ SEQUENCE 784 AA; 89639 MW; F36311C4063B2075 CRC64;  
 Query Match 86.7%; Score 26; DB 1; Length 784;  
 Best Local Similarity 100.0%; Pred. No. 2.3e-02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 VDVEY 6  
 DB 739 VDVEY 743  
 RESULT 42  
 SYTB\_THETN STANDARD; PRT; 794 AA.  
 AC Q8R9C7;  
 DT 15-SEP-2003 (Rel. 42, Created)  
 DT 15-SEP-2003 (Rel. 42, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE Phenylalanyl-tRNA synthetase beta chain (EC 6.1.1.20)  
 DE (Phenylalanine--tRNA ligase beta chain) (PHERS).  
 GN PHET OR TTE1588.  
 OS Thermoanaerobacter tengcongensis.  
 OC Bacteria; Firmicutes; Clostridia; Thermoanaerobacteriales;  
 OC Thermoanaerobacteriaceae; Thermoanaerobacter.  
 OX NCBI\_TaxID=119072;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=MB4 / JCM 11007;  
 RX MEDLINE=21992816; PubMed=11997336;  
 RA Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J.,  
 RA Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling L.,  
 RA Tan H., Chen R., Wang J., Yu J., Yang H.;  
 RT "A complete sequence of T. tengcongensis genome.";  
 RL Genome Res. 12:689-700(2002).  
 CC -!- CATALYTIC ACTIVITY: ATP + L-phenylalanine + tRNA(Phe) = AMP +  
 CC diphosphate + L-phenylalanyl-tRNA(Phe).  
 CC -!- COFACTOR: Binds 2 magnesium ions per tetramer (By similarity).  
 CC -!- SUBUNIT: Tetramer of two alpha and two beta chains (By  
 CC similarity).  
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -!- SIMILARITY: Belongs to the phenylalanyl-tRNA synthetase beta chain  
 CC family. Subfamily 1.  
 CC -!- SIMILARITY: Contains 1 tRNA-binding domain.  
 CC -----  
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 CC -----  
 DR EMBL; AE013123; AAM24889.1; -  
 DR HAMAP; MF\_00283; -; 1  
 DR InterPro; IPR005146; B3\_4.  
 DR InterPro; IPR005147; B5.  
 DR InterPro; IPR005121; Fdx-AntiCB.  
 DR InterPro; IPR004532; PheT\_bact.  
 DR InterPro; IPR002547; tRNA\_bind.  
 DR Pfam; PF03483; B3\_4; 1.  
 DR Pfam; PF03484; B5; 1.  
 DR Pfam; PF03147; FDX-ACB; 1.  
 DR Pfam; PF01588; tRNA\_bind; 1.  
 DR TIGRfams; TIGR00472; pheT\_bact; 1.  
 DR PROSITE; PS0886; TRBD; 1.  
 KW Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;  
 KW Metal-binding; Magnesium; RNA-binding; tRNA-binding;  
 KW Complete proteome.  
 FT DOMAIN 39 152 TRNA-BINDING.  
 FT METAL 457 457 MAGNESIUM (BY SIMILARITY).  
 FT METAL 463 463 MAGNESIUM (VIA CARBONYL OXYGEN) (BY  
 FT METAL 466 466 SIMILARITY).  
 FT METAL 467 467 MAGNESIUM (BY SIMILARITY).  
 FT METAL 467 467 MAGNESIUM (BY SIMILARITY).  
 SQ SEQUENCE 794 AA; 88954 MW; F9179929B0461A7F CRC64;  
 Query Match 86.7%; Score 26; DB 1; Length 794;  
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 VDVEY 6  
 DB 630 VDVEY 634  
 RESULT 43  
 VP3\_BT10 STANDARD; PRT; 901 AA.  
 ID VP1\_BT10  
 AC P12435;  
 DT 01-OCT-1999 (Rel. 12, Created)  
 DT 01-OCT-1999 (Rel. 12, Last sequence update)



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CC -----
CC EMBL; L19969; AAA42846.1; -
CC HSSP; P56582; 2BTU
CC InterPro; IPR002614; Orbi_VP3.
CC Pfam; PF01700; Orbi_VP3; 1.
CC ProDom; PD004438; Orbi_VP3; 1.
CC Core protein.
CC SEQUENCE 901 AA; 103405 MW; 2C81F5D7CA304D0D CRC64;
CC -----
Query Match 86.7%; Score 26; DB 1; Length 901;
Best Local Similarity 66.7%; Pred. No. 2.6e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 SVDVEY 6
DB 454 TIDVEY 459
-----
RESULT 45
VP3_BT13 STANDARD; PRT; 901 AA.
ID VP3_BT13
AC Q65750;
DT 15-DEC-1998 (Rel. 37, Created)
DD 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE VP3 core protein (Major inner capsid protein).
DS S3 OR L3.
OS Bluetongue virus (serotype 13 / isolate USA).
OC Viruses; dsRNA viruses; Reoviridae; Orbivirus.
OX NCBI_TaxID=33717;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94360628; PubMed=8079518;
RT "Hwang G.-Y., Xiang M., Li J.K.-K.;
RT "Analysis and conservation of sequences among the cognate L3 segments
RT of the five United States bluetongue viruses.";
RL Virus Res. 32:381-389(1994).
CC -1- FUNCTION: THE VP3 PROTEIN IS ONE OF THE FIVE PROTEINS (WITH VP1,
CC VP4, VP6 AND VP7) WHICH FORM THE INNER CAPSID OF THE VIRUS.
CC -1- SIMILARITY: BELONGS TO THE REOVIRUSES VP3 FAMILY.
CC -----
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CC -----
CC EMBL; L19969; AAA42847.1; -
CC HSSP; P56582; 2BTU.
CC InterPro; IPR002614; Orbi_VP3.
CC Pfam; PF01700; Orbi_VP3; 1.
CC ProDom; PD004438; Orbi_VP3; 1.
CC Core protein.
CC SEQUENCE 901 AA; 103369 MW; F37A56AD3AF2A768 CRC64;
CC -----
Query Match 86.7%; Score 25; DB 1; Length 901;
Best Local Similarity 66.7%; Pred. No. 2.6e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 SVDVEY 6
DB 454 TIDVEY 459

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RESULT 46
VP3_BT17
ID _VP3_BT17 STANDARD; PRT; 901 AA.
AC P03539;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE VP3 core protein (Major inner capsid protein).
GN S3 OR L3.
OS Bluetongue virus (serotype 17 / isolate USA).
OC Viruses; dsRNA viruses; Reoviridae; Orbivirus.
OX NCBI_TaxID=33718;
RN [1]
SEQUENCE FROM N.A.
RP MEDLINE=84292453; PubMed=6206233;
RA Purdy M.A., Petre J., Roy P.;
RT "Cloning of the bluetongue virus L3 gene.";
RL J. Virol. 51:754-759(1984).
RN [2]
SEQUENCE FROM N.A.
RP MEDLINE=85242823; PubMed=2989873;
RA Roy P., Purdy M.A., Petre J., Rao C.D.;
RT "Cloning and nucleotide sequencing of bluetongue virus genomes.";
RL Prog. Clin. Biol. Res. 178:363-370(1985).
CC -1- FUNCTION: THE VP3 PROTEIN IS ONE OF THE FIVE PROTEINS (WITH VP1,
VP4, VP6 AND VP7) WHICH FORM THE INNER CAPSID OF THE VIRUS.
CC -1- SIMILARITY: BELONGS TO THE REOVIRUSES VP3 FAMILY.
CC -----
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CC -----
DR EMBL; K02369; AAA42831.1; -
DR EMBL; M32722; AAA42839.1; -
DR PIR; A04148; P3XR17.
DR HSSP; P56582; 2BTU.
DR InterPro; IPR002614; Orbi_VP3.
DR Pfam; PF01700; Orbi_VP3; 1.
DR ProDom; PD004438; Orbi_VP3; 1.
KW Core protein.
SQ SEQUENCE 901 AA; 103414 MW; C93F110D9C313A3C CRC64;

Query Match 86.7%; Score 26; DB 1; Length 901;
Best Local Similarity 66.7%; Pred. No. 2.6e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVEY 6
Db 454 TIDVEY 459

RESULT 47
VP3_BT1A
ID _VP3_BT1A STANDARD; PRT; 901 AA.
AC F20608;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE VP3 core protein (Major inner capsid protein).
GN S3 OR L3.
OS Bluetongue virus (serotype 1 / isolate Australia).
OC Viruses; dsRNA viruses; Reoviridae; Orbivirus.
OX NCBI_TaxID=10904;
RN [1]
SEQUENCE FROM N.A.
RP MEDLINE=87236783; PubMed=3035818;
RA Gould A.R.;
RT "The complete nucleotide sequence of bluetongue virus serotype 1 RNA3
RT and a comparison with other geographic serotypes from Australia,

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RT South Africa and the United States of America, and with other
RT orbivirus isolates.";
RL Virus Res. 7:169-183(1987).
CC -1- FUNCTION: THE VP3 PROTEIN IS ONE OF THE FIVE PROTEINS (WITH VP1,
VP4, VP6 AND VP7) WHICH FORM THE INNER CAPSID OF THE VIRUS.
CC -1- SIMILARITY: BELONGS TO THE REOVIRUSES VP3 FAMILY.
DR HSSP; P56582; 2BTU.
DR InterPro; IPR002614; Orbi_VP3.
DR Pfam; PF01700; Orbi_VP3; 1.
DR ProDom; PD004438; Orbi_VP3; 1.
KW Core protein.
SQ SEQUENCE 901 AA; 103205 MW; 12312208188C1206 CRC64;

Query Match 86.7%; Score 26; DB 1; Length 901;
Best Local Similarity 66.7%; Pred. No. 2.6e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVEY 6
Db 454 TIDVEY 459

RESULT 48
VP3_BT1S
ID _VP3_BT1S STANDARD; PRT; 901 AA.
AC P56582;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE VP3 core protein (Major inner capsid protein).
GN S3 OR L3.
OS Bluetongue virus (serotype 1 / isolate South Africa).
OC Viruses; dsRNA viruses; Reoviridae; Orbivirus.
OX NCBI_TaxID=10905;
RN [1]
X-RAY CRYSTALLOGRAPHY (3.5 ANGSTROMS).
RX MEDLINE=98445087; PubMed=9774103;
RA Grimes J.M., Burroughs J.N., Gouet P., Diprose J.M., Malby R.,
RA Zientara S., Merrens P.P., Stuart D.I.;
RT "The atomic structure of the bluetongue virus core.";
RL Nature 395:470-478(1998).
CC -1- FUNCTION: THE VP3 PROTEIN IS ONE OF THE FIVE PROTEINS (WITH VP1,
VP4, VP6 AND VP7) WHICH FORM THE INNER CAPSID OF THE VIRUS.
CC -1- SIMILARITY: BELONGS TO THE REOVIRUSES VP3 FAMILY.
DR InterPro; IPR002614; Orbi_VP3.
DR Pfam; PF01700; Orbi_VP3; 1.
DR ProDom; PD004438; Orbi_VP3; 1.
KW Core protein; 3D-structure.
FT TURN 9 11
FT HELIX 16 18
FT STRAND 22 26
FT HELIX 28 47
FT TURN 48 49
FT HELIX 64 72
FT TURN 73 76
FT STRAND 90 94
FT STRAND 101 105
FT HELIX 106 112
FT TURN 113 113
FT HELIX 123 141
FT STRAND 146 146
FT STRAND 150 153
FT TURN 154 155
FT STRAND 156 159
FT HELIX 161 163
FT STRAND 166 167
FT TURN 169 171
FT HELIX 172 174
FT HELIX 177 187
FT TURN 188 189
FT STRAND 191 191
FT TURN 193 194

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FT TURN 196 197  
FT STRAND 202 204  
FT HELIX 211 226  
FT STRAND 229 245  
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FT STRAND 269 280  
FT HELIX 275 280  
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FT STRAND 353 356  
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FT HELIX 497 506  
FT HELIX 510 535  
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FT HELIX 541 543  
FT HELIX 546 558  
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FT STRAND 567 570  
FT HELIX 573 580  
FT TURN 581 581  
FT STRAND 585 588  
FT TURN 591 595  
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FT HELIX 634 643  
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FT TURN 660 660  
FT HELIX 663 671  
FT STRAND 678 678  
FT HELIX 679 691  
FT TURN 692 693  
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FT STRAND 699 699  
FT STRAND 703 709  
FT HELIX 718 721  
FT TURN 725 726  
FT STRAND 731 731  
FT HELIX 738 740  
FT STRAND 741 744  
FT HELIX 746 754  
FT TURN 755 756  
FT HELIX 758 767

FT TURN 768 769  
FT STRAND 771 774  
FT STRAND 780 786  
FT HELIX 792 795  
FT TURN 796 796  
FT STRAND 801 802  
FT STRAND 815 816  
FT STRAND 821 826  
FT TURN 832 833  
FT HELIX 836 839  
FT STRAND 846 851  
FT STRAND 858 861  
FT TURN 864 865  
FT HELIX 866 869  
FT TURN 870 871  
FT STRAND 875 877  
FT TURN 879 880  
FT STRAND 882 885  
FT TURN 892 893  
FT STRAND 896 896  
SQ SEQUENCE 901 AA; 103181 MW; B89384F344AE3669 CRC64;

Query Match 86.7%; Score 26; DB 1; Length 901;  
Best Local Similarity 66.7%; Pred. No. 2.6e+02;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVEY 6  
Db 454 TIDVEY 459

RESULT 49

VP3\_BT2A  
ID\_VP3\_BT2A STANDARD; PRT; 901 AA.  
AC Q65748;  
DT 15-DEC-1998 (Rel. 37, Created)  
DT 15-DEC-1998 (Rel. 37, Last sequence update)  
DT 15-DEC-1998 (Rel. 37, Last annotation update)  
DE VP3 core protein (Major inner capsid protein).  
GN S3 OR L3.  
OS Bluetongue virus (serotype 2 / isolate USA).  
OC Viruses; dsRNA viruses; Reoviridae; Orbivirus.  
OX NCBI\_TaxID=10907;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=94360628; PubMed=8079518;  
RA Huang G.-Y., Xiang M., Li J.K.-K.;  
RT "Analyses and conservation of sequences among the cognate L3 segments of the five United States bluetongue viruses.";  
RL Virus Res. 32:381-389(1994).  
CC -I- FUNCTION: THE VP3 PROTEIN IS ONE OF THE FIVE PROTEINS (WITH VP1, VP4, VP6 AND VP7) WHICH FORM THE INNER CAPSID OF THE VIRUS.  
CC -I- SIMILARITY: BELONGS TO THE REOVIRUSES VP3 FAMILY.  
CC -----  
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CC -----  
CC EMBL; L19967; AAA88825.1; -.  
DR HSSP; P56582; 2BTV.  
DR InterPro; IPR002614; Orbi\_VP3.  
DR Pfam; PF01700; Orbi\_VP3; 1.  
DR ProDom; PD004438; Orbi\_VP3; 1.  
KW Core protein.  
SQ SEQUENCE 901 AA; 103224 MW; DA2B7E589B252462 CRC64;  
  
Query Match 86.7%; Score 26; DB 1; Length 901;  
Best Local Similarity 66.7%; Pred. No. 2.6e+02;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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QY      1 SVDVEY 6
DB      454 TIDVEY 459

RESULT 50
RPC2_HUMAN
ID      RPC2_HUMAN      STANDARD;      PRT;      1133 AA.
AC      Q9NW08; O9NW59;
DT      15-SEP-2003 (Rel. 42, Created)
DT      15-SEP-2003 (Rel. 42, Last sequence update)
DE      DNA-directed RNA polymerase III subunit 127.6 kDa polypeptide
DE      (SC 2.7.7.6) (RNA polymerase III subunit 2) (RPC2).
GN      POLR3B.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=22278866; PubMed=12391170;
RA      Hu P., Wu S., Sun Y., Yuan C.-C., Kobayashi R., Myers M.P.,
RA      Hernandez N.;
RT      "Characterization of human RNA polymerase III identifies orthologues
RT      for Saccharomyces cerevisiae RNA polymerase III subunits.";
RL      Mol. Cell. Biol. 22:8044-8055(2002).
RN      [2]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Muscle;
RX      MEDLINE=22388257; PubMed=12477932;
RA      Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA      Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA      Altschul S.F., Zeng H., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA      Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA      Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA      Stapleton M., Soares M.B., Bonaldo M.F., Cavaant T.L., Scheetz T.E.,
RA      Brownstein M.J., Udgin T.B., Teshiyuki S., Carninci P., Prange C.,
RA      Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA      Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA      Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA      Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA      Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA      Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA      Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA      Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA      Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA      Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT      "Generation and initial analysis of more than 15,000 full-length
RT      human and mouse cDNA sequences";
RL      Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN      [3]
RP      SEQUENCE OF 751-1133 FROM N.A.
RC      TISSUE=Teratocarcinoma;
RA      Isogai T., Ota T., Hayaishi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA      Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
RA      Wagtsuma M., Hosoiri T., Raku Y., Kodaira H., Kondo H., Sugawara M.,
RA      Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,
RA      Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
RA      Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,
RA      Ninomiya K., Iwavanagi T.;
RT      "NEDO human cDNA sequencing project.";
RL      Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
CC      -!- FUNCTION: DNA-dependent RNA polymerase catalyzes the transcription
CC      of DNA into RNA using the four ribonucleoside triphosphates as
CC      substrates.
CC      -!- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
CC      [RNA] (N).
CC      -!- SUBUNIT: RNA polymerase III consists of about 15 different
CC      subunits. This subunit is the second largest component of RNA
CC      polymerase III.
CC      -!- SUBCELLULAR LOCATION: Nuclear.

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-!- SIMILARITY: Belongs to the RNA polymerase beta chain family.  
 -----  
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 or send an email to [license@ebi-sib.ch](mailto:license@ebi-sib.ch)).  
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 EMBL; AY02084; AAM18214.1; -  
 EMBL; BC046238; AHA46238.1; -  
 EMBL; AK001161; BAA91527.1; ALT\_INIT.  
 EMBL; AK001250; BAA91581.1; ALT\_INIT.  
 InterPro; IPR001572; RNA\_pol\_B.  
 Pfam; PF00562; RNA\_pol\_Rpb2\_6; 1.  
 Pfam; PF04560; RNA\_pol\_Rpb2\_7; 1.  
 PROSITE; PS01166; RNA\_POL\_BETA; 1.  
 Transferrase; DNA-directed RNA polymerase; Transcription; Zinc;  
 Zinc-finger; Nuclear protein.  
 ZN\_FING 1080 1095 C4-TYPE (POTENTIAL).  
 FT CONFLICT 258 258 E -> A (IN REF. 1).  
 FT CONFLICT 978 978 R -> C (IN REF. 3; BAA91527).  
 SQ SEQUENCE 1133 AA; 127784 MW; F0B3AFF892DDED7D CRC64;  
  
 Query Match 86.7%; Score 26; DB 1; Length 1133;  
 Best Local Similarity 66.7%; Pred. No. 3.3e+02;  
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 1 SVDVEY 6  
 DB 114 TIDVEY 119  
  
 Search completed: January 20, 2004, 13:55:20  
 Job time : 13 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 20, 2004, 13:54:52 ; Search time 36 Seconds  
(without alignments)  
43.009 Million cell updates/sec

Title: US-09-919-703-1  
Perfect score: 30  
Sequence: 1 SVDVEY 6

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues  
Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 75 summaries

- Database : SPTREMBL\_23.\*
- 1: sp\_archaea.\*
  - 2: sp\_bacteria.\*
  - 3: sp\_fungi.\*
  - 4: sp\_human.\*
  - 5: sp\_invertebrate.\*
  - 6: sp\_mammal.\*
  - 7: sp\_mhc.\*
  - 8: sp\_organelle.\*
  - 9: sp\_plant.\*
  - 10: sp\_rodent.\*
  - 11: sp\_virus.\*
  - 12: sp\_vertebrate.\*
  - 13: sp\_unclassified.\*
  - 14: sp\_rviro.\*
  - 15: sp\_bacteriap.\*
  - 16: sp\_archaeap.\*
  - 17: sp\_mhc.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	30	100.0	157	16 Q8YF57	Q8YF57 bruceella me
2	30	100.0	157	16 Q8G2R4	Q8G2R4 bruceella su
3	30	100.0	279	10 Q49899	Q49899 medicago sa
4	30	100.0	414	2 Q53284	Q53284 streptococc
5	30	100.0	891	5 Q25177	Q25177 hydra atten
6	30	100.0	1041	16 Q8PHD3	Q8PHD3 xanthomonas
7	30	100.0	1041	16 Q8P613	Q8P613 xanthomonas
8	30	100.0	1274	10 F93125	F93125 dunaliella
9	29	96.7	60	5 Q9NFR4	Q9NFR4 drosophila
10	29	96.7	74	16 Q9LSP9	Q9LSP9 salmonella
11	29	96.7	186	5 O16567	O16567 caenorhabdi
12	29	96.7	215	16 Q97B84	Q97B84 clostridium
13	29	96.7	360	16 Q8CWI5	Q8CWI5 wigglewort
14	29	96.7	547	5 Q8WSF9	Q8WSF9 aplysia cal
15	29	96.7	615	3 Q9P861	Q9P861 axula aden
16	29	96.7	830	2 Q9AGP8	Q9AGP8 arthrobacte

17	29	96.7	836	10 Q9FGN0	Q9fgn0 aradiopsis
18	29	96.7	862	5 Q8IL36	Q8il36 plasmodium
19	29	96.7	1154	5 Q27492	Q27492 caenorhabdi
20	29	96.7	1595	2 Q52373	Q52373 caldicellul
21	29	96.7	2473	5 Q8MMK4	Q8mmk4 dictyosteli
22	28	93.3	146	9 Q8SCX2	Q8scx2 pseudomonas
23	28	93.3	148	2 Q9ADW6	Q9adw6 ehrlichia c
24	28	93.3	387	16 Q8FU72	Q8fu72 corynebacte
25	28	93.3	433	12 Q8V3P9	Q8v3p9 swinepox vi
26	28	93.3	579	5 Q23355	Q23355 caenorhabdi
27	28	93.3	907	5 Q9U3Q5	Q9u3q5 caenorhabdi
28	27	90.0	136	12 Q12377	Q12377 marek's dis
29	27	90.0	180	5 Q9J968	Q9j968 caenorhabdi
30	27	90.0	210	12 Q8JJY6	Q8jjy6 spodoptera
31	27	90.0	213	10 Q8H275	Q8h275 oryza sativ
32	27	90.0	271	16 Q8X2B1	Q8x2b1 escherichia
33	27	90.0	271	16 Q8X298	Q8x298 escherichia
34	27	90.0	275	10 Q9FWF3	Q9fwf3 oryza sativ
35	27	90.0	277	17 Q9HKV3	Q9hkv3 thermoplas
36	27	90.0	279	10 Q8LGS6	Q8lgs6 oryza sativ
37	27	90.0	289	10 Q8LSQ4	Q8lsg4 oryza sativ
38	27	90.0	302	12 Q993F5	Q993f5 callitrichi
39	27	90.0	307	17 Q8ZTC7	Q8ztc7 pyrobaculum
40	27	90.0	320	11 Q8BNF3	Q8bnf3 mus musculu
41	27	90.0	349	16 Q9L074	Q9l074 streptomyce
42	27	90.0	355	2 P71435	P71435 leptospira
43	27	90.0	355	2 Q48587	Q48587 leptospira
44	27	90.0	368	2 Q47904	Q47904 fusobacteri
45	27	90.0	368	2 Q47903	Q47903 fusobacteri
46	27	90.0	368	16 Q8RHY1	Q8rhy1 fusobacteri
47	27	90.0	370	2 Q47905	Q47905 fusobacteri
48	27	90.0	372	2 Q47913	Q47913 fusobacteri
49	27	90.0	374	16 Q8F8E1	Q8f8e1 leptospira
50	27	90.0	375	16 Q8X4C8	Q8x4c8 escherichia
51	27	90.0	391	3 Q12132	Q12132 saccharomyc
52	27	90.0	391	12 Q89268	Q89268 gallid herp
53	27	90.0	399	16 Q05452	Q05452 mycobacteri
54	27	90.0	405	17 Q8U2Q0	Q8u2q0 pyrococcus
55	27	90.0	407	16 Q8X5F6	Q8x5f6 escherichia
56	27	90.0	409	5 Q8MMR8	Q8mmr8 dictyosteli
57	27	90.0	437	16 Q8X5D0	Q8x5d0 escherichia
58	27	90.0	437	16 Q9EVE8	Q9eve8 escherichia
59	27	90.0	438	16 Q8X3D6	Q8x3d6 escherichia
60	27	90.0	439	16 Q8XEG4	Q8xeg4 escherichia
61	27	90.0	439	16 Q8X5B4	Q8x5b4 escherichia
62	27	90.0	439	16 Q8X5A7	Q8x5a7 escherichia
63	27	90.0	440	16 Q8X3W0	Q8x3w0 escherichia
64	27	90.0	496	2 Q8RMB9	Q8rmb9 thermotoga
65	27	90.0	515	5 Q9VXK9	Q9vdx9 drosophila
66	27	90.0	518	16 Q8XTS6	Q8xts6 ralatonia s
67	27	90.0	555	16 Q8FI57	Q8fi57 escherichia
68	27	90.0	572	2 Q9RP94	Q9rp94 streptococc
69	27	90.0	573	5 Q8TOR9	Q8tor9 drosophila
70	27	90.0	621	16 Q9JXR3	Q9jxr3 neisseria m
71	27	90.0	621	16 Q9JW59	Q9jw59 neisseria m
72	27	90.0	622	2 Q31248	Q31248 acinetobact
73	27	90.0	687	16 Q8FIF4	Q8fif4 escherichia
74	27	90.0	766	9 Q80245	Q80245 mycoplasma
75	27	90.0	809	16 Q8FEX7	Q8fex7 escherichia

ALIGNMENTS

RESULT 1  
Q8YF57 PRELIMINARY; PRT; 157 AA.  
ID Q8YF57  
AC Q8YF57;  
DT 01-MAR-2002 (T-EMBLrel. 20, Created)  
DT 01-MAR-2002 (T-EMBLrel. 20, Last sequence update)  
DE 01-JUN-2002 (T-EMBLrel. 21, Last annotation update)  
GN Arsenate reductase.  
GN BMEI1670.

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OS Brucella melitensis.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Brucellaceae; Brucella.
OX NCBI_TaxID=29459;
RN [1];
RP SEQUENCE FROM N.A.
RC STRAIN=16M / ATCC 23456 / Biotype 1;
RA MEDLINE=20020109; PubMed=11756688;
RA DelVecchio V.G., Kapatral V., Redkar R.J., Patra G., Mijer C., Los T.,
RA Ivanova N., Anderson I., Bhattacharyya A., Lykidis A., Reznik G.,
RA Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goltsman E.,
RA Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J.,
RA Haselkorn R., Kyriades N., Overbeek R.;
RT "The genome sequence of the facultative intracellular pathogen
RT Brucella melitensis";
RL Proc. Natl. Acad. Sci. U.S.A. 99:443-448(2002).
DR EMBL; AE009602; AAL52851.1; -.
DR InterPro; IPR000106; Low_mwt_FTPase.
DR Pfam; PF01451; LMWPC; 1.
DR SMART; SM00226; LMWPC; 1.
DR Complete proteome.
SQ SEQUENCE 157 AA; 17446 MW; D8AA7748107ECB65 CRC64;

Query Match 100.0%; Score 30; DB 16; Length 157;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVEY 6
Db 114 SVDVEY 119

RESULT 2
Q8G2R4 PRELIMINARY; PRT; 157 AA.
ID Q8G2R4;
AC Q8G2R4;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DE Protein phosphatase, putative.
GN BR0250.
OS Brucella suis.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Brucellaceae; Brucella.
OX NCBI_TaxID=29461;
RN [1];
RP SEQUENCE FROM N.A.
RC STRAIN=1330 / Biovar 1;
RX MEDLINE=2247741; PubMed=12271122;
RA Paulsen I.T., Seshadri R., Nelson K.E., Eisen J.A., Heidelberg J.F.,
RA Read T.D., Dodson R.J., Umayam L., Brinkac L.M., Beanan M.J.,
RA Daugherty S.C., Deboy R.T., Durkin A.S., Kolonay J.F., Madupu R.,
RA Nelson W.C., Ayodeji B., Kraul M., Shetty J., Malek J., Van Aken S.E.,
RA Riedmuller S., Tettelin H., Gill S.R., White O., Salzberg S.L.,
RA Hoover D.L., Lindler L.E., Halling S.M., Boyle S.M., Fraser C.M.;
RT "The Brucella suis genome reveals fundamental similarities between
RT animal and plant pathogens and symbionts";
RL Proc. Natl. Acad. Sci. U.S.A. 99:13148-13153(2002).
DR EMBL; AE014338; AAN29199.1; -.
DR TIGR; BR0250; -.
DR Complete proteome.
SQ SEQUENCE 157 AA; 17446 MW; D8AA7748107ECB65 CRC64;

Query Match 100.0%; Score 30; DB 16; Length 157;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVEY 6
Db 114 SVDVEY 119

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O49899 PRELIMINARY; PRT; 279 AA.
ID O49899;
AC O49899;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Lectin precursor.
GN LEC2.
OS Medicago sativa (Alfalfa).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae; Medicago.
OX NCBI_TaxID=3879;
RN [1];
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Chief;
RA Brill L.M., Pieterse V.R.;
RT "Legume seed lectin genes: sequence of Mslec2 from Alfalfa, Alfalfa
RT and Sweet Clover southern blot analysis, and stable transformation of
RT Alfalfa with antisense-lectin constructs.";
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; Y16754; CAA76366.1; -.
DR HSP; P04122; 1LOE.
DR InterPro; IPR000985; Lectin_legA.
DR InterPro; IPR001220; Lectin_legB.
DR Pfam; PF00138; lectin_legA; 1.
DR Pfam; PF00139; lectin_legB; 1.
DR ProDom; PD000671; Lectin_legA; 1.
DR ProDom; PD000711; Lectin_legB; 1.
DR PROSITE; PS00308; LECTIN_LEGUME_ALPHA; 1.
DR PROSITE; PS00307; LECTIN_LEGUME_BETA; 1.
KW Signal.
FT SIGNAL 1 25 POTENTIAL.
FT CHAIN 26 279 LECTIN.
SQ SEQUENCE 279 AA; 30551 MW; 1315F022BABDA360 CRC64;

Query Match 100.0%; Score 30; DB 10; Length 279;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVEY 6
Db 208 SVDVEY 213

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RESULT 4
Q53284 PRELIMINARY; PRT; 414 AA.
ID Q53284;
AC Q53284;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE SKC-2.
OS Streptococcus equisimilis.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=119602;
RN [1];
RP SEQUENCE FROM N.A.
RA MEDLINE=93000998; PubMed=1368792;
RA Estrada M.P., Hernandez L., Perez A., Rodriguez P., Serrano R.,
RA Rubiera R., Pedraza A., Padron G., Antuch W., de la Fuente J.,
RA Herrera L.;
RT "High level expression of streptokinase in Escherichia coli.";
RL Biotechnology 10:1138-1142(1992).
DR EMBL; S46536; AAC60418.1; -.
DR InterPro; IPR004093; Staphylokinase.
DR Pfam; PF02821; Staphylokinase; 3.
SQ SEQUENCE 414 AA; 47254 MW; F75BE5831B766904 CRC64;

Query Match 100.0%; Score 30; DB 2; Length 414;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 SVDVEY 6  
Db 157 SVDVEY 162

RESULT 5  
Q25177 PRELIMINARY; PRT; 891 AA.

AC Q25177;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Receptor protein-tyrosine kinase (fragment).  
OS Hydra attenuata (Hydra) (Hydra vulgaris).  
OC Eukaryota; Metazoa; Chnidaria; Hydrozoa; Hydrozoa; Anthomedusae;  
OC Hydridae; Hydra.  
OX NCBI\_TaxID=6087;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=UCI;  
RA Chen R.L., Steele R.E.;  
RL Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.  
DR EMBL; U24116; AAA65223.1; -  
DR HSSP; P11362; 1PGK.  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig MHC.  
DR InterPro; IPR000719; Prot\_kinase.  
DR InterPro; IPR001245; Tyr\_kinase.  
DR Pfam; PF00047; Ig; 2.  
DR Pfam; PF00069; pkinase; 1.  
DR PRINTS; PR00109; TYRKINASE.  
DR ProDom; PD000001; Prot\_kinase; 1.  
DR SMART; SM00409; IG; 1.  
DR SMART; SM00219; TyKc; 1.  
DR PROSITE; PS00835; IG-LIKE; 2.  
DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.  
DR PROSITE; PS00109; PROTEIN KINASE TYR; 1.  
KW ATP-binding; Kinase; Transferase; Tyrosine-protein kinase.  
FT NON\_TER 891  
SQ SEQUENCE 891 AA; 100976 MW; 1CFDF4BCCA298176 CRC64;

Query Match 100.0%; Score 30; DB 5; Length 891;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVEY 6  
Db 137 SVDVEY 142

RESULT 6  
Q25177 PRELIMINARY; PRT; 1041 AA.

AC Q25177;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
DE Acriflavin resistance protein.  
GN ACRF OR XAC3326.  
OS Xanthomonas axonopodis (pv. citri).  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;  
OC Xanthomonadaceae; Xanthomonas.  
OX NCBI\_TaxID=92829;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=306 / ATCC 13902 / XV 101;  
RX MEDLINE=22022145; PubMed=12024217;  
RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,  
Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,  
Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,  
Camarotte G., Cannavan F., Cardozo J., Chambergo F., Ciapina L.P.,  
Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorri H.,  
Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,  
Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,  
Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,  
Locati E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,  
Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,  
Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,  
Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,  
Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,  
Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,  
Setubal J.C., Kitajima J.P.;  
RL "Comparison of the genomes of two Xanthomonas pathogens with differing host specificities."  
RT host specificities;  
RL Nature 417:459-463(2002).  
DR EMBL; AE012433; AAM42439.1; -  
DR InterPro; IPR001036; Acrlflavin\_res.  
DR Pfam; PF00873; ACR\_tran; 1.  
DR PRINTS; PR00702; ACRIFLAVINRP.  
KW Complete proteome.  
SQ SEQUENCE 1041 AA; 112760 MW; 09DD20F99B7217F8 CRC64;

Query Match 100.0%; Score 30; DB 16; Length 1041;

RA Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorri H.,  
Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,  
Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,  
Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,  
Locati E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,  
Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,  
Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,  
Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,  
Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,  
Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,  
Setubal J.C., Kitajima J.P.;  
RL "Comparison of the genomes of two Xanthomonas pathogens with differing host specificities."  
RT host specificities;  
RL Nature 417:459-463(2002).  
DR EMBL; AE012433; AAM42439.1; -  
DR InterPro; IPR001036; Acrlflavin\_res.  
DR Pfam; PF00873; ACR\_tran; 1.  
DR PRINTS; PR00702; ACRIFLAVINRP.  
KW Complete proteome.  
SQ SEQUENCE 1041 AA; 112474 MW; 091A63B63E31E12 CRC64;

Query Match 100.0%; Score 30; DB 16; Length 1041;  
Best Local Similarity 100.0%; Pred. No. 2.2e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVEY 6  
Db 46 SVDVEY 51

RESULT 7  
Q25177 PRELIMINARY; PRT; 1041 AA.

AC Q25177;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
DE Acriflavin resistance protein.  
GN ACRF OR XCC3169.  
OS Xanthomonas campestris (pv. campestris).  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;  
OC Xanthomonadaceae; Xanthomonas.  
OX NCBI\_TaxID=340;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=ATCC 33913 / NCPPB 528;  
RX MEDLINE=22022145; PubMed=12024217;  
RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,  
Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,  
Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,  
Camarotte G., Cannavan F., Cardozo J., Chambergo F., Ciapina L.P.,  
Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorri H.,  
Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,  
Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,  
Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,  
Locati E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,  
Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,  
Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,  
Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,  
Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,  
Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,  
Setubal J.C., Kitajima J.P.;  
RL "Comparison of the genomes of two Xanthomonas pathogens with differing host specificities."  
RT host specificities;  
RL Nature 417:459-463(2002).  
DR EMBL; AE012433; AAM42439.1; -  
DR InterPro; IPR001036; Acrlflavin\_res.  
DR Pfam; PF00873; ACR\_tran; 1.  
DR PRINTS; PR00702; ACRIFLAVINRP.  
KW Complete proteome.  
SQ SEQUENCE 1041 AA; 112760 MW; 09DD20F99B7217F8 CRC64;

Query Match 100.0%; Score 30; DB 16; Length 1041;

Best Local Similarity 100.0%; Pred. No. 2.2e+02; Mismatches 0; Indels 0; Gaps 0;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVEY 6  
 |||||  
 Db 46 SVDVEY 51

RESULT 8  
 P93125 PRELIMINARY; PRT; 1274 AA.  
 AC P93125;  
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)  
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Ttf-1.  
 GN TTF1  
 OS Dunaliella salina.  
 OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;  
 OC Dunaliellaceae; Dunaliella.  
 OX NCBI\_TaxID=3046;  
 [1] \_  
 RN SEQUENCE FROM N.A.  
 RA Fisher M., Gokhman I., Pick U., Zamir A.;  
 RL Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; U77059; AAB36531.1; -;  
 DR HSSP; P56410; LAOV.  
 DR InterPro; IPR001156; Transferrin.  
 DR Pfam; PF00405; transferrin; 5.  
 DR PRINTS; PRO0422; TRANSFERRIN.  
 DR SMART; SM00094; TR\_FER; 1.  
 SQ SEQUENCE 1274 AA; 136668 MW; 6C2EE9D914097699 CRC64;

Query Match 100.0%; Score 30; DB 10; Length 1274;  
 Best Local Similarity 100.0%; Pred. No. 2.7e+02; Mismatches 0; Indels 0; Gaps 0;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVEY 6  
 |||||  
 Db 1186 SVDVEY 1191

RESULT 9  
 Q9NFR4 PRELIMINARY; PRT; 60 AA.  
 AC Q9NFR4;  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Nicotinic acetylcholine receptor Dalpha 4 subunit (Fragment).  
 GN NACR-ALPHA-80B OR NACRALPHA-80B OR CG12414 OR CG17552.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_TaxID=7227;  
 [1] \_  
 RN SEQUENCE FROM N.A.  
 RA Lansdel S.J., Millar N.S.;  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.  
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.  
 DR EMBL; AJ272160; CAB77446.1; -;  
 DR FlyBase; FBGN0037212; nacr-alpha-80B.  
 DR InterPro; IPR006201; Neur\_channel.  
 DR InterPro; IPR006202; Neur\_chan\_LBD.  
 DR Pfam; PF02931; Neur\_chan\_LBD; 1.  
 DR PROSITE; PS00236; NEUROTR ION CHANNEL; 1.  
 KW Glycoprotein; Ionic channel; Postsynaptic membrane; Receptor;  
 KW Transmembrane.  
 FT NON\_TER 1  
 FT NON\_TER 60  
 FT NON\_TER 60  
 SQ SEQUENCE 60 AA; 6868 MW; E3A9483419FAD0C6 CRC64;

Query Match 96.7%; Score 29; DB 5; Length 60;  
 Best Local Similarity 83.3%; Pred. No. 18; Mismatches 1; Indels 0; Gaps 0;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVEY 6  
 |||||  
 Db 34 SVDVEY 39

RESULT 10  
 Q9LSP9 PRELIMINARY; PRT; 74 AA.  
 AC Q9LSP9;  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
 DE Orf, hypothetical protein (Hypothetical 8.2 kDa protein).  
 GN R0092 OR HCM1.13C.  
 OS Salmonella typhi.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Salmonella.  
 OX NCBI\_TaxID=601;  
 [1] \_  
 RN SEQUENCE FROM N.A.  
 RA Sherburne C.K., Lawley T.D., Gilmour M.W., Blattner F.R., Burland V.,  
 RA Grobeck E., Rose D.J., Taylor D.E.;  
 RT "The complete DNA sequence and analysis of R27, a large IncHI plasmid  
 from Salmonella typhi that is temperature sensitive for transfer.";  
 RL Nucleic Acids Res. 28:2177-2186(2000).  
 [2]  
 RN SEQUENCE FROM N.A.  
 RC STRAIN=CT18; PLASMID=PHCM1;  
 RX MEDLINE=21534947; PubMed=11677608;  
 RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,  
 RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M.,  
 RA Baker S., Basham D., Brooks K., Chillingworth T., Connor P.,  
 RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,  
 RA Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,  
 RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,  
 RA Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,  
 RA Whitehead S., Barrall B.G.;  
 RT "Complete genome sequence of a multiple drug resistant Salmonella  
 RT enterica serovar Typhi CT18.";  
 RL Nature 413:848-852(2001).  
 DR EMBL; AF250878; AAF69930.1; -;  
 DR EMBL; AL513383; CAD09627.1; -;  
 KW Hypothetical protein; Plasmid; Complete proteome.  
 SQ SEQUENCE 74 AA; 8199 MW; DCC7A8A73B746EAF CRC64;

Query Match 96.7%; Score 29; DB 16; Length 74;  
 Best Local Similarity 83.3%; Pred. No. 23; Mismatches 1; Indels 0; Gaps 0;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVEY 6  
 |||||  
 Db 30 SVDVEY 35

RESULT 11  
 O16567 PRELIMINARY; PRT; 186 AA.  
 AC O16567;  
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)  
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE B0047.4 protein.  
 GN B0047.4  
 OS Caenorhabditis elegans.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;



DR	InterPro; IPR005834; Hydrolase.
DR	Pfam; PF00702; Hydrolase; 1.
DR	PRINTS; PR00413; HADHALOGENASE.
DR	TIGRFAMS; TIGR01509; HAD-SF-IA-v3; 1.
KW	Complete proteome.
SQ	SEQUENCE 215 AA; 24421 MW; C4334F6313CBFC15 CRC64;
 Query Match 96.7%; Score 29; DB 16; Length 215; Best Local Similarity 83.3%; Pred. No. 71; Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps	
Qy	1 SVDVEY 6
Db	25 SIDVEY 30
 RESULT 13	
Q8CW15	PRELIMINARY; PRT; 360 AA.
ID	Q8CW15
AC	Q8CW15;
DT	01-MAR-2003 (TrEMBLrel. 23, Created)
DT	01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DE	01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DD	Heme protein.
DN	[1]
GN	HEME.
OS	Wigglesworthia brevipalpis.
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OX	Enterobacteriaceae; Wigglesworthia.
NCBI_TaxID=164509;	
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=2297718; PubMed=12219091;
RA	Akman L., Yamashita A., Watanabe H., Oshima K., Shiba T., Hattori M.,
RA	Aksoy S.;
RT	"Genome sequence of the endocellular obligate symbiont of tsetse
RL	flies, Wigglesworthia glossinidia.";
RL	Nat. Genet. 32:402-407(2002).
DR	EMBL; AB063522; BAC24654.1; -.
KW	Complete proteome.
SQ	SEQUENCE 360 AA; 41359 MW; CA18CB13C1B8492B CRC64;
 Query Match 96.7%; Score 29; DB 16; Length 360; Best Local Similarity 83.3%; Pred. No. 1.2e+02; Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps	
Qy	1 SVDVEY 6
Db	272 SVDIEY 277
 RESULT 14	
Q8NSP9	PRELIMINARY; PRT; 547 AA.
ID	Q8NSP9
AC	Q8NSP9;
DT	01-MAR-2002 (TrEMBLrel. 20, Created)
DT	01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DE	01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DD	Non-alpha nicotinic acetylcholine receptor subunit.
OS	Aplysia californica (California sea hare).
OC	Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC	Apogastropoda; Heterobranchia; Euthyneura; Opisthobranchia; Anaspidaea
OC	Aplysioides; Aplysiidae; Aplysia.
NCBI_TaxID=6500;	
RN	[1]
RP	SEQUENCE FROM N.A.
RA	Sadreyev R.I., Panchin Y.V., Meleshkevich E.A., Moroz L.L.;
RT	"Non-alpha nicotinic acetylcholine receptor subunit from the
RT	individual identified neurons of Aplysia californica";
CC	Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
CC	-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC	-!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
DR	EMBL; AF322876; AAL37250.1; -.
DR	InterPro; IPR006201; Neur channel.

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DR InterPro; IPR006202; Neur_chan_LBD.
DR InterPro; IPR006029; Neu_Channel_memb.
DR Pfam; PF02931; Neur_chan_LBD; 1.
DR Pfam; PF02932; Neur_chan_memb; 1.
DR PRINTS; PR00252; NRIONCHANNEL.
DR TIGRFAMs; TIGR00860; LIC; 1.
DR PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
DR Glycoprotein; Ionic channel; Postsynaptic membrane; Receptor;
KW Transmembrane.
SQ SEQUENCE 547 AA; 62535 MW; 3D3F01D78605C91 CRC64;

Query Match 96.7%; Score 29; DB 5; Length 547;
Best Local Similarity 83.3%; Pred. No. 1.9e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVEY 6
Db 155 SIDVEY 160

RESULT 15
Q9P861 PRELIMINARY; PRT; 615 AA.
AC Q9P861
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Ferro-O2-oxidoreductase precursor.
GN AFET3.
OS Arxula adeninivorans.
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Dipodascaceae; mitosporic Dipodascaceae; Arxula.
OX NCBI_TaxID=37620;

[1]
SEQUENCE FROM N.A.
RC STRAIN=LS3;
RA Wantenfel R., Stoltenburg R., Kunze G.;
RA "Post-translational modifications of the AFET3 gene product - a
RT component of iron transport system in budding cells and mycelia of the
RT yeast Arxula adeninivorans LS3."
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ277833; CAB90817.1; -.
DR HSSP; P37064; 1A0Z.
DR InterPro; IPR001117; Cu-oxidase.
DR InterPro; IPR002355; MultiCu oxidase2.
DR Pfam; PF00394; Cu-oxidase; 3.
DR PROSITE; PS00079; MULTICOPPER_OXIDASE1; 1.
DR PROSITE; PS00080; MULTICOPPER_OXIDASE2; 1.
KW Signal.
FT SIGNAL 1 17 POTENTIAL.
FT CHAIN 18 615 FERRO-O2-OXIDOREDUCTASE.
SQ SEQUENCE 615 AA; 69624 MW; 79200D42A28715E4 CRC64;

Query Match 96.7%; Score 29; DB 3; Length 615;
Best Local Similarity 83.3%; Pred. No. 2.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVEY 6
Db 311 SIDVEY 316

RESULT 16
Q9AGP8 PRELIMINARY; PRT; 830 AA.
AC Q9AGP8
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-NAR-2003 (TrEMBLrel. 23, Last annotation update)
DE N,N-dimethylglycine oxidase.
GN DMG.
OS Arthrobacter globiformis.

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OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Micrococcineae; Micrococcaceae; Arthrobacter.
OX NCBI_TaxID=1665;

[1]
SEQUENCE FROM N.A.
RC STRAIN=NRRL B-2979;
RA Meskys R., Harris R.J., Casate V., Bastran J., Scrutton N.S.;
RT "Genetic organization of the genes involved in dimethylglycine and
RT sarcosine degradation in Arthrobacter spp.: implications for glycine
RT betaine catabolism."
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF329477; AAK16482.1; -.
DR InterPro; IPR006222; GCV_T.
DR InterPro; IPR006076; IPR006076.
DR InterPro; IPR000205; NAD_binding.
DR Pfam; PF01266; DAO; 1.
DR Pfam; PF01571; GCV_T; 1.
SQ SEQUENCE 830 AA; 89984 MW; 13DE3C4B3DF325DA CRC64;

Query Match 96.7%; Score 29; DB 2; Length 830;
Best Local Similarity 83.3%; Pred. No. 3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVEY 6
Db 801 SIDVEY 806

RESULT 17
Q9FGN0 PRELIMINARY; PRT; 836 AA.
AC Q9FGN0
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Similarity to unknown protein.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosid II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;

[1]
SEQUENCE FROM N.A.
RC STRAIN=Columbia;
RA Kaneko T., Katoh T., Asamizu E., Sato S., Nakamura Y., Kotani H.,
RA Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 5. XI."
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB025621; BAB09754.1; -.
SQ SEQUENCE 836 AA; 92259 MW; A875BAE2F18F61BD CRC64;

Query Match 96.7%; Score 29; DB 10; Length 836;
Best Local Similarity 83.3%; Pred. No. 3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVEY 6
Db 772 SIDVEY 777

RESULT 18
Q8IL36 PRELIMINARY; PRT; 862 AA.
AC Q8IL36
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein.
GN Pf4_0413.
OS Plasmodium falciparum (isolate 3D7).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=36329;

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Query Match	96.7%;	Score 29;	DB 5;	Length 1154;
Best Local Similarity	83.3%;	Pred. No. 4.2e+02;		
Matches	5;	Conservative	1;	Mismatches 0; Indels 0; Gaps 0;
Qy	1	SVDVEY 6		
Db	117	SVDIEY 122		
RESULT 20				
O52373		PRELIMINARY;	PRT;	1595 AA.
ID	O52373			
AC	O52373;			
DT	01-JUN-1998 (TReMBLrel. 06, Created)			
DT	01-JUN-1998 (TReMBLrel. 06, Last sequence update)			
DT	01-MAR-2003 (TReMBLrel. 23, Last annotation update)			
DE	Family 10 xylanase (EC 3.2.1.8).			
DE	Family 10 xylanase (EC 3.2.1.8).			
GN	XYNB.			
OS	Caldicellulosiruptor sp. Rt59B.1.			
OC	Bacteria; Firmicutes; Clostridia; Clostridiales; Syntrophomonadaceae;			
OC	Caldicellulosiruptor.			
CX	NCBI_TaxID=70295;			
CX	[1]			
RP	SEQUENCE FROM N.A.			
RP	STRAIN=Rc69B.1;			
RA	Morris D.D., Gibbs M.D., Ford M., Thomas J., Bergquist P.L.;			
RT	"Family 10 and 11 xylanase genes from Caldicellulosiruptor sp.			
RT	Rt69B.1.";			
RL	Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.			
CC	-1- SIMILARITY: BELONGS TO CELLULASE FAMILY F (FAMILY 10 OF GLYCOSYL			
CC	HYDROLASES).			
CC	EMBL; AF036923; AAB95325.1; -.			
DR	HSSP; P23360; 1K6A.			
DR	InterPro; IPR003305; CBM_CenC.			
DR	InterPro; IPR001000; Glyco_Hydro_10.			
DR	InterPro; IPR001119; SLH.			
DR	Pfam; PF02018; CBM 4_9; 3.			
DR	Pfam; PF00331; Glyco_Hydro_10; 1.			
DR	Pfam; PF00395; SLH; 3.			
DR	PRINTS; PR00134; GLHYDRLASE10.			
DR	SMART; SM00633; Glyco 10; 1.			
DR	PROSITE; PS00591; GLYCOSYL_HYDROL_F10; 1.			
KW	Glycosidase; Hydrolase; Xylan degradation.			
SEQ	SEQUENCE 1595 AA; 178404 MW; EC31B2363F30EFSB CRC64;			
Query Match	96.7%;	Score 29;	DB 2;	Length 1595;
Best Local Similarity	83.3%;	Pred. No. 6e+02;		
Matches	5;	Conservative	1;	Mismatches 0; Indels 0; Gaps 0;
Qy	1	SVDVEY 6		
Db	1548	SIDVEY 1553		
RESULT 21				
Q8MMK4		PRELIMINARY;	PRT;	2473 AA.
ID	Q8MMK4			
AC	Q8MMK4;			
DT	01-OCT-2002 (TReMBLrel. 22, Created)			
DT	01-OCT-2002 (TReMBLrel. 22, Last sequence update)			
DT	01-MAR-2003 (TReMBLrel. 23, Last annotation update)			
DE	Dicogen synthase (EC 2.4.1.21).			
DE	Dictyostelium discoideum (slime mold).			
OC	Eukaryota; Mycetozoa; Dictyostellida; Dictyostelium.			
OC	NCBI_TaxID=44689;			
RP	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=AX;			
RA	Lehmann G., Eichinger L., Szafranski K., Pachebat J., Dear P.,			
RA	Glockner R., Baumgart C., Parra G., April J.F., Guigo R., Kumpf K.,			
RA	Tunggal B., Cox E., Quail M.A., Platzer M., Rosenthal A., Noegel A.A.;			
RA	"Sequence and Analysis of Chromosome 2 of Dictyostelium.";			
RL	Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.			

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DR EMBL; AC117082; AAM34363.1; -.
SQ SEQUENCE 2473 AA; 274970 MW; 6395FD78B45A7945 CRC64;

Query Match
Best Local Similarity 96.7%; Score 29; DB 5; Length 2473;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVEY 6
Db 999 SVDIEY 1004

RESULT 22
Q8SCX2 PRELIMINARY; PRT; 146 AA.
AC Q8SCX2
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE PHIK2190.
OS Pseudomonas phage phiK2.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae.
OX NCBI_TaxID=169683;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=21914557; PubMed=11916376;
RA Mesyanzhinov V.V., Robben J., Grymonprez B., Kostyuchenko V.A.,
RA Bourkaltseva M.V., Sykilinda N.N., Krylov V.V., Voickaert G.;
RA Bourkaltseva M.V., Sykilinda N.N., Krylov V.N., Voickaert G.;
RT "The genome of bacteriophage phiK2 of Pseudomonas aeruginosa.";
RL J. Mol. Biol. 317:1-19(2002).
RN [2]
RP SEQUENCE FROM N.A.
RA Mesyanzhinov V.V., Robben J., Grymonprez B., Kostyuchenko V.A.,
RA Bourkaltseva M.V., Sykilinda N.N., Krylov V.V., Voickaert G.;
RA SubMITTED (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF399011; AAL83091.1; -.
DR InterPro; IPR001596; Pyrophosphatase.
DR PROSITE; PS00387; PPASE; 1.
SQ SEQUENCE 146 AA; 17037 MW; A1584AF76C9EAC13 CRC64;

Query Match
Best Local Similarity 93.3%; Score 28; DB 9; Length 146;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVEY 6
Db 94 SVDIEY 99

RESULT 23
Q9ADW6 PRELIMINARY; PRT; 148 AA.
AC Q9ADW6
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Hypothetical 17.6 kDa protein.
OS Ehrlichia canis.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
OC Anaplasmataceae; Ehrlichia.
OX NCBI_TaxID=944;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=Oklahoma;
RX MEDLINE=98371112; PubMed=9705412;
RA Ohashi N., Unver A., Zhi N., Rikihisa Y.;
RT "Cloning and characterization of multigenes encoding the
RT immunodominant 30-kilodalton major outer membrane proteins of
RT Ehrlichia canis and application of the recombinant protein for
RT serodiagnosis.";
RL J. Clin. Microbiol. 36:2671-2680(1998).
RN [2]
RP SEQUENCE FROM N.A.
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RT "The genome of swinepox virus.";  
RL J. Virol. 76:783-790(2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=17077-99;  
RA Alfonso C.L., Tulman E.R., Lu Z., Balinsky C., Osorio F.A., Zsak L.,  
RC Kutish G.F., Rock D.L.;  
EA Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.  
RL EMBL; AF410153; AAL69784.1; -;  
DR InterPro; IPR004970; Peptidase\_C57.  
DR Pfam; PF03290; Peptidase\_C57; 1.  
SQ SEQUENCE 433 AA; 51052 MW; 2F9F7F0CE436A7D8 CRC64;  
  
Query Match 93.3%; Score 28; DB 12; Length 433;  
Best Local Similarity 66.7%; Pred. No. 2.6e+02;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 SVDVEY 6  
Db 388 SIDIEY 393  
  
RESULT 26  
Q23355 PRELIMINARY; PRT; 579 AA.  
ID Q23355  
AC Q23355;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE ZC504.2 protein.  
GN ZC504.2.  
OS Caenorhabditis elegans.  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
OC Rhabditidae; Peloderinae; Caenorhabditis.  
OX NCBI\_TaxID=6239;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Kershaw J.K.;  
RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=99069613; PubMed=9851916;  
RA none;  
RT "Genome sequence of the nematode C.elegans: A platform for  
RT investigating biology.";  
RL Science 282:2012-2018(1998).  
DR EMBL; Z83216; CAB62784.1; -;  
DR HSP; O53752; IPI1; CE23529.  
DR WormPep; C08F11.14; IPI1; CE23529.  
DR InterPro; IPR006254; Isocit\_lyase.  
DR InterPro; IPR000918; Isocit\_lyase.ph.  
DR InterPro; IPR006252; Malate\_synthA.  
DR InterPro; IPR001465; Malate\_synthase.  
DR Pfam; PF00463; ICL; 1.  
DR Pfam; PF01274; Malate\_synthase; 1.  
DR ProDom; PD001857; Isocit\_lyase.ph; 1.  
DR TIGRFAMs; TIGR01346; isocit\_lyase; 1.  
DR TIGRFAMs; TIGR01344; malate\_synthA; 1.  
DR PROSITE; PS00161; ISOCITRATE\_LYASE; 1.  
SQ SEQUENCE 907 AA; 101848 MW; AAF64B820B82D1B9 CRC64;  
  
Query Match 93.3%; Score 28; DB 5; Length 907;  
Best Local Similarity 66.7%; Pred. No. 5.7e+02;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 SVDVEY 6  
Db 18 SIDIEY 23  
  
RESULT 28  
O12377 PRELIMINARY; PRT; 136 AA.  
ID O12377  
AC O12377;  
DT 01-JUL-1997 (TrEMBLrel. 04, Created)  
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Protein kinase like-protein (Fragment).  
GN PK.  
OS Marek's disease virus serotype 2 MDV2.  
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;  
OC Alphaherpesvirinae; Marek's disease-like viruses.  
OX NCBI\_TaxID=36353;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=97128994; PubMed=8973534;  
RA Jang H.K., Ono M., Kato Y., Tohya Y., Niihara M., Mikami T.;  
RT "Identification of a potential Marek's disease virus serotype 2  
RT glycoprotein D gene with homology to herpes simplex virus glycoprotein  
RT D.";  
RL Arch. Virol. 141:2207-2216(1996).  
DR EMBL; S83367; AAB50855.1; -;  
DR InterPro; IPR000719; Prot\_kinase.  
DR Pfam; PF00069; pkinase; 1.  
DR ProDom; PD000001; Prot\_kinase; 1.  
DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
KW ATP-binding; Kinase; transferase.  
FT NON\_TER 1  
SQ SEQUENCE 136 AA; 15535 MW; D6B9F39529DD5D3A CRC64;

DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE C08F11.14 protein.  
GN C08F11.14  
OS Caenorhabditis elegans.  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
OC Rhabditidae; Peloderinae; Caenorhabditis.  
OX NCBI\_TaxID=6239;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Matthews L.;  
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=99069613; PubMed=9851916;  
RA none;  
RT "Genome sequence of the nematode C.elegans: A platform for  
RT investigating biology.";  
RL Science 282:2012-2018(1998).  
DR EMBL; Z83216; CAB62784.1; -;  
DR HSP; O53752; IPI1; CE23529.  
DR WormPep; C08F11.14; IPI1; CE23529.  
DR InterPro; IPR006254; Isocit\_lyase.  
DR InterPro; IPR000918; Isocit\_lyase.ph.  
DR InterPro; IPR006252; Malate\_synthA.  
DR InterPro; IPR001465; Malate\_synthase.  
DR Pfam; PF00463; ICL; 1.  
DR Pfam; PF01274; Malate\_synthase; 1.  
DR ProDom; PD001857; Isocit\_lyase.ph; 1.  
DR TIGRFAMs; TIGR01346; isocit\_lyase; 1.  
DR TIGRFAMs; TIGR01344; malate\_synthA; 1.  
DR PROSITE; PS00161; ISOCITRATE\_LYASE; 1.  
SQ SEQUENCE 907 AA; 101848 MW; AAF64B820B82D1B9 CRC64;  
  
Query Match 93.3%; Score 28; DB 5; Length 907;  
Best Local Similarity 66.7%; Pred. No. 5.7e+02;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 SVDVEY 6  
Db 18 SIDIEY 23  
  
RESULT 28  
O12377 PRELIMINARY; PRT; 136 AA.  
ID O12377  
AC O12377;  
DT 01-JUL-1997 (TrEMBLrel. 04, Created)  
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Protein kinase like-protein (Fragment).  
GN PK.  
OS Marek's disease virus serotype 2 MDV2.  
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;  
OC Alphaherpesvirinae; Marek's disease-like viruses.  
OX NCBI\_TaxID=36353;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=97128994; PubMed=8973534;  
RA Jang H.K., Ono M., Kato Y., Tohya Y., Niihara M., Mikami T.;  
RT "Identification of a potential Marek's disease virus serotype 2  
RT glycoprotein D gene with homology to herpes simplex virus glycoprotein  
RT D.";  
RL Arch. Virol. 141:2207-2216(1996).  
DR EMBL; S83367; AAB50855.1; -;  
DR InterPro; IPR000719; Prot\_kinase.  
DR Pfam; PF00069; pkinase; 1.  
DR ProDom; PD000001; Prot\_kinase; 1.  
DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
KW ATP-binding; Kinase; transferase.  
FT NON\_TER 1  
SQ SEQUENCE 136 AA; 15535 MW; D6B9F39529DD5D3A CRC64;

Query Match 90.0%; Score 27; DB 12; Length 136;  
 Best Local Similarity 83.3%; Pred. No. 1.3e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVEY 6  
 Db 92 SMDVEY 97  
 |:|||||

RESULT 29  
 Q09968 PRELIMINARY; PRT; 180 AA.  
 ID Q09968  
 AC Q09968;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Hypothetical 20.6 kDa protein.  
 GN B0244.9  
 OS Caenorhabditis elegans.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
 OC Rhabditidae; Peleoderinae; Caenorhabditis.  
 OX NCBI\_TaxID=6239;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Bristol N2;  
 RX MEDLINE=99069613; PubMed=9851916;  
 RA None;  
 RT "Genome sequence of the nematode C. elegans: a platform for  
 RT investigating biology. The C. elegans Sequencing Consortium.";  
 RL Science 282:2012-2018(1998).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Bristol N2;  
 RA Favello A.;  
 RT "The sequence of C. elegans cosmid B0244.";  
 RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Bristol N2;  
 RA Waterston R.;  
 RT "Direct Submission.";  
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; U28971; AAA68377.1; -  
 DR WormPep; B0244.9; CE01756  
 DR InterPro; IPR001865; Ribosomal S2.  
 DR PROSITE; PS00962; RIBOSOMAL\_S2\_1; 1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 180 AA; 20592 MW; 9B41BA9212622FD4 CRC64;

Query Match 90.0%; Score 27; DB 5; Length 180;  
 Best Local Similarity 83.3%; Pred. No. 1.8e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVEY 6  
 Db 8 SVDLEY 13  
 |:|||||

RESULT 30  
 Q8JJY6 PRELIMINARY; PRT; 210 AA.  
 ID Q8JJY6  
 AC Q8JJY6;  
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Thymidine kinase.  
 OS Spodoptera frugiperda ascovirus 1.  
 OC Viruses; dsDNA viruses, no RNA stage; Ascoviridae; Ascovirus.  
 OX NCBI\_TaxID=113374;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=a;

RA Stasiak K., Renault S., Demattei M.V., Bigot Y., Federici B.A.;  
 RT "Evolution of Ascoviruses from Iridoviruses";  
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AJ312690; CAC84464.1; -  
 DR InterPro; IPR002624; dNK.  
 DR Pfam; PF01712; dNK; 1.  
 KW Kinase.  
 SQ SEQUENCE 210 AA; 24522 MW; 9B28484AF10C6B79 CRC64;

Query Match 90.0%; Score 27; DB 12; Length 210;  
 Best Local Similarity 83.3%; Pred. No. 2.1e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVEY 6  
 Db 160 SLDVEY 165  
 |:|||||

RESULT 31  
 Q8H275 PRELIMINARY; PRT; 213 AA.  
 ID Q8H275  
 AC Q8H275;  
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Expansin-like protein (Fragment).  
 OS Oryza sativa (japonica cultivar-group).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC Ehrhartoideae; Oryzae; Oryza.  
 OX NCBI\_TaxID=39947;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=23315554; PubMed=12428004;  
 RA Lee Y., Kende H.;  
 RT "Expression of alpha-Expansin and Expansin-Like Genes in Deepwater  
 RT Rice.";  
 RL Plant Physiol. 130:1396-1405(2002).  
 DR EMBL; AY100693; AAMS2409.1; -  
 FT NON\_TER 1  
 SQ SEQUENCE 213 AA; 23205 MW; F2AB23F4E257C70B CRC64;

Query Match 90.0%; Score 27; DB 10; Length 213;  
 Best Local Similarity 83.3%; Pred. No. 2.1e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVEY 6  
 Db 80 AVDVEY 85  
 |:|||||

RESULT 32  
 Q8X2B1 PRELIMINARY; PRT; 271 AA.  
 ID Q8X2B1  
 AC Q8X2B1;  
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Putative tail fiber protein encoded within prophage CP-933V.  
 GN Z3309.  
 OS Escherichia coli O157:H7.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Escherichia.  
 OX NCBI\_TaxID=83334;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=O157:H7 / EDL933 / ATCC 700927;  
 RX MEDLINE=21074935; PubMed=11206551;  
 RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,  
 RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,  
 RA Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,  
 RA Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamocis K.,  
 RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,

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RA Welch R.A., Blattner F.R.;
RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
RL Nature 403:529-533(2001).
DR EMBL; AE005440; AAG57198.1; -.
KW Complete proteome.
SQ SEQUENCE 271 AA; 27706 MW; CB4DSCB197B93B1B CRC64;

Query Match 90.0%; Score 27; DB 16; Length 271;
Best Local Similarity 83.3%; Pred. No. 2.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVDVEY 6
|:|||||
Db 52 SMDVEY 57

RESULT 33
Q8X298 PRELIMINARY; PRT; 271 AA.
AC Q8X298;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Putative tail fiber protein.
GN ECS2159.
OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=83334;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=O157:H7 / RIMD 0509952;
RX MEDLINE=21156231; PubMed=11258796;
RA Hayashi T., Makino K., Kurokawa K., Ishii K., Yokoyama K.,
RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
RA Iida T., Takami H., Honda T., Sasaki C., Ogasawara N., Yasunaga T.,
RA Kuhara S., Shiba T., Hattori M., Shinagawa H.;
RT "Complete genome sequence of enterohemorrhagic Escherichia coli
RT O157:H7 and genomic comparison with a laboratory strain K-12.";
RL DNA Res. 8:11-22(2001).
DR EMBL; AP002557; BAB35582.1; -.
SQ SEQUENCE 271 AA; 28057 MW; AA7AC4F3A9F8B7F4 CRC64;

Query Match 90.0%; Score 27; DB 16; Length 271;
Best Local Similarity 83.3%; Pred. No. 2.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVDVEY 6
|:|||||
Db 52 SMDVEY 57

RESULT 34
Q9FWF3 PRELIMINARY; PRT; 275 AA.
AC Q9FWF3;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Putative pollen allergen.
GN OSJNB001511.10.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Elmhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=cv. Nipponbare;
RA Buell C.R., Yuan Q., Moffat K.S., Hill J.N., Jenkins C.N., Burr P.C.,
RA Hsiao J., Zismann V., Pai G., Bowman C.L., Fujii C.Y., VanAken S.E.,
RA Bowman C.L., Craven B., Uterback T.R., Khalak H., Feldblyum T.V.,
RA Quackenbush J., White O., Salzberg S.L., Fraser C.M.;

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RT "Oryza sativa chromosome 10 BAC OSJNB00151111 genomic sequence.";
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
CC 1- SIMILARITY: BELONGS TO THE EXPANSIN FAMILY.
DR EMBL; AC051633; RAG13596.1; -.
DR Gramene; Q9FWF3; -.
DR InterPro; IPR007112; Expan_endogl.
DR InterPro; IPR007118; Expan_Lol_pi.
DR InterPro; IPR007117; Expan_Lol_pi_C.
DR Pfam; PF01357; Pollen allergen; 1.
DR PRINTS; PR01225; EXPANSINFAMILY.
DR ProDom; PD002179; Expan_Lol_pi_C; 1.
DR PROSITE; PS00843; EXPANSIN_CBD; 1.
DR PROSITE; PS00842; EXPANSIN_EG45; 1.
SQ SEQUENCE 275 AA; 29301 MW; E088C7DF0596A1C7 CRC64;

Query Match 90.0%; Score 27; DB 10; Length 275;
Best Local Similarity 83.3%; Pred. No. 2.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVDVEY 6
|:|||||
Db 141 AVDVEY 146

RESULT 35
Q9HKV3 PRELIMINARY; PRT; 277 AA.
AC Q9HKV3;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical protein Ta0490.
GN TA0490.
OS Thermoplasma acidophilum.
OC Archaea; Euryarchaeota; Thermoplasmata; Thermoplasmatales;
OC Thermoplasmataceae; Thermoplasma.
OX NCBI_TaxID=2303;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=DSM 1728;
RX MEDLINE=20479972; PubMed=11029001;
RA Ruepp A., Graml W., Santos-Martinez M.-L., Koretke K.K., Volker C.,
RA Mewes H.-W., Frishman D., Stocker S., Lupas A.N., Baumeister W.;
RT "The genome sequence of the thermoacidophilic scavenger Thermoplasma
RT acidophilum.";
RL Nature 407:508-513(2000).
DR EMBL; AL445064; CAC11632.1; -.
DR InterPro; IPR002035; VWF_A.
DR SMART; SM00327; VWA; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 277 AA; 31081 MW; 7DB9492F1A735CD6 CRC64;

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Query Match 90.0%; Score 27; DB 17; Length 277;
Best Local Similarity 83.3%; Pred. No. 2.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVDVEY 6
|:|||||
Db 113 TVDVEY 118

RESULT 36
Q8LGS6 PRELIMINARY; PRT; 279 AA.
AC Q8LGS6;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Expansin-like protein 1.
GN EXPL1.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

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OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RA Lee Y., Kende H.;
RT "Expression of expansin-like genes in rice internodes.";
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE EXPANSIN FAMILY.
DR EMBL; AY039022; AAK84681.1; -.
DR Gramene; Q8LS66; -.
DR InterPro; IPR007112; Expan_endogl.
DR InterPro; IPR007118; Expan_Lol_pi.
DR InterPro; IPR007117; Expan_Lol_pi_C.
DR Pfam; PF01357; Pollen_allergen; 1.
DR PRINTS; PR01225; EXPANSNFAMLY.
DR PRODOM; PD002179; Expan_Lol_pi_C; 1.
DR PROSITE; PS0843; EXPANSIN_CBD; 1.
DR PROSITE; PS0842; EXPANSIN_EG45; 1.
SQ SEQUENCE 279 AA; 30038 MW; FD9B86A5A6A9BA2B CRC64;

Query Match 90.0%; Score 27; DB 10; Length 279;
Best Local Similarity 83.3%; Pred. No. 2.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVDVEY 6
Db 146 AVDVEY 151

RESULT 37
Q8LSQ4
ID Q8LSQ4 PRELIMINARY; PRT; 289 AA.
AC Q8LSQ4;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 22, Last annotation update)
DE Putative pollen allergen.
GN OJ1004C08.4.
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RA Wang R.A., Yu Y., Soderlund C., Chen M., Kim H.-R., Rambo T.,
RA Saski C., Henry D., Oates R., Simmons J.;
RT "Rice Genomic Sequence.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE EXPANSIN FAMILY.
DR EMBL; AC098693; AAM22698.1; -.
DR Gramene; Q8LSQ4; -.
DR InterPro; IPR007112; Expan_endogl.
DR InterPro; IPR007118; Expan_Lol_pi.
DR InterPro; IPR007117; Expan_Lol_pi_C.
DR Pfam; PF01357; Pollen_allergen; 1.
DR PRINTS; PR01225; EXPANSNFAMLY.
DR PRODOM; PD002179; Expan_Lol_pi_C; 1.
DR PROSITE; PS0843; EXPANSIN_CBD; 1.
DR PROSITE; PS0842; EXPANSIN_EG45; 1.
SQ SEQUENCE 289 AA; 31238 MW; 5EF4D782A7EF7322 CRC64;

Query Match 90.0%; Score 27; DB 10; Length 289;
Best Local Similarity 83.3%; Pred. No. 2.9e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVDVEY 6
Db 146 AVDVEY 151

RESULT 38
Q993F5
ID Q993F5 PRELIMINARY; PRT; 302 AA.
AC Q993F5;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE CRF54.
OS Callitriche herpesvirus 3.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Gammaherpesvirinae; Lymphocryptovirus.
OX NCBI_TaxID=106331;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CJ0149;
RX MEDLINE=21107697; PubMed=11158621;
RA Cho Y., Ramer J., Rivailier P., Quink C., Garber R.L., Beier D.R.,
RA Wang F.;
RT "An Epstein-Barr-related herpesvirus from marmoset lymphomas.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:1224-1229(2001).
DR EMBL; AF319782; AAK38263.1; -.
DR InterPro; IPR00358; Ribonucl_redctse.
DR Pfam; PF00268; ribonuc_red_sm_1.
DR PROSITE; PS00368; RIBORED_SMALL; 1.
SQ SEQUENCE 302 AA; 34794 MW; 48FCFD543F4028F0 CRC64;

Query Match 90.0%; Score 27; DB 12; Length 302;
Best Local Similarity 83.3%; Pred. No. 3.1e-02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVDVEY 6
Db 221 AVDVEY 226

RESULT 39
Q8ZTC7
ID Q8ZTC7 PRELIMINARY; PRT; 307 AA.
AC Q8ZTC7;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE D-3-phosphoglycerate dehydrogenase (serA).
GN PAE3320.
OS Pyrobaculum aerophilum.
OC Archaea; Crenarchaeota; Thermoprotei; Thermoproteales;
OC Thermoproteaceae; Pyrobaculum.
OX NCBI_TaxID=13773;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IM2 / ATCC 51768 / DSM 7523;
RX PubMed=11792869;
RA Fitz-Gibbon S.T., Ladner H., Kim U.-J., Stetter K.O., Simon M.I.,
RA Miller J.H.;
RT "Genome sequence of the hyperthermophilic crenarchaeon Pyrobaculum
RL aerophilum.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:984-989(2002).
DR EMBL; AE009924; AAL64835.1; -.
DR InterPro; IPR006139; 2-Hacid_DH.
DR InterPro; IPR006140; 2-Hacid_DH_C.
DR Pfam; PF00389; 2-Hacid_DH; 1.
DR Pfam; PF02826; 2-Hacid_DH_C; 1.
DR PROSITE; PS00670; D_2-HYDROXYACID_DH_2; 1.
DR PROSITE; PS00671; D_2-HYDROXYACID_DH_3; 1.
KW Complete proteome.
SQ SEQUENCE 307 AA; 33783 MW; 07134831A775D358 CRC64;

Query Match 90.0%; Score 27; DB 17; Length 307;
Best Local Similarity 83.3%; Pred. No. 3.1e-02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVDVEY 6
Db 76 NVDVEY 81
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RESULT 40
Q8BNF3 PRELIMINARY; PRT; 320 AA.
AC Q8BNF3; 2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Ceroid-lipofuscinosis.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Dorsal root ganglion;
RX MEDLINE=22354693; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
DR EMBL; AK083832; BAC39034.1; -.
SQ SEQUENCE 320 AA; 34522 MW; 91DC3FBF778631C8 CRC64;

Query Match 90.0%; Score 27; DB 11; Length 320;
Best Local Similarity 83.3%; Pred. No. 3.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVDVEY 6
:|||||
Db 31 SLDVEY 36

RESULT 41
Q9L074 PRELIMINARY; PRT; 349 AA.
AC Q9L074;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Putative secreted protein.
GN SCO2780 OR SCC105.11.
OS Streptomyces coelicolor.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA Brown S.P., Harris D.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA Cerdeno A.M., Parkhill J., Barrell B.G., Rajandream M.A.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RX MEDLINE=97000351; PubMed=8843436;
RA Redenbach M., Kieser H.M., Denapite D., Bichner A., Cullum J.,
RA Kinashi H., Hopwood D.A.;
RT "A set of ordered cosmids and a detailed genetic and physical map for
RT the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
RL Mol. Microbiol. 21:77-96 (1996).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2) / M145;
RX MEDLINE=21996410; PubMed=12000953;
RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
RA Thomson N.R., James K.D., Harris D.B., Quail M.A., Kieser H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,

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RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neill S.,
RA Rabinowitch E., Rajandream M.A., Rutherford K., Rutter S.,
RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
RA Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
RA Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
RT coelicolor A3(2).";
RL Nature 417:141-147 (2002).
DR EMBL; AL939113; CAB87217.1; -.
DR InterPro; IPR002491; Peripla BP.
DR Pfam; PF01497; Peripla_BP_2; 1.
KW Complete proteome.
SQ SEQUENCE 349 AA; 36642 MW; 2E3B2A72B6BF780A CRC64;

Query Match 90.0%; Score 27; DB 16; Length 349;
Best Local Similarity 83.3%; Pred. No. 3.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVDVEY 6
:|||||
Db 243 SVDLEY 248

RESULT 42
P71435 PRELIMINARY; PRT; 355 AA.
AC P71435;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Outer membrane lipoprotein.
GN LPP41.
OS Leptospira interrogans.
OC Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.
OX NCBI_TaxID=173;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=serovar pomona;
RA Morris K.K.;
RL Thesis (1995), University of California, Davis.
DR EMBL; U31426; AAB09404.1; -.
DR InterPro; IPR001440; TPR.
KW Lipoprotein.
SQ SEQUENCE 355 AA; 38952 MW; 4CC8837D81BF3412 CRC64;

Query Match 90.0%; Score 27; DB 2; Length 355;
Best Local Similarity 83.3%; Pred. No. 3.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVDVEY 6
:|||||
Db 23 TVDVEY 28

RESULT 43
Q48587 PRELIMINARY; PRT; 355 AA.
AC Q48587;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE LipL41 protein precursor.
GN LIPL41.
OS Leptospira kirschneri.
OC Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.
OX NCBI_TaxID=29507;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RM52;
RX MEDLINE=96239055; PubMed=8675344;
RA Shang E.S., Summers T.A., Haake D.A.;
RT "Molecular cloning and sequence analysis of the gene encoding LipL41,

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a surface-exposed lipoprotein of pathogenic *Leptospira* species.";  
 RT Infect. Immun. 64:2322-2330(1996).  
 RL EMBL; L46794; AAB06799.1; -.  
 DR InterPro; IPR001440; TPR.  
 KW Signal.  
 FT SIGNAL 19 POTENTIAL.  
 FT CHAIN 20 355 POTENTIAL.  
 SQ SEQUENCE 355 AA; 38910 MW; 89D2EA08D271DC78 CRC64;  
 Query Match 90.0%; Score 27; DB 2; Length 355;  
 Best Local Similarity 83.3%; Pred. No. 3.6e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SVDVEY 6  
 Db 23 TVDVEY 28  
 RESULT 44  
 Q47904 PRELIMINARY; PRT; 368 AA.  
 ID Q47904  
 AC Q47904;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Outer membrane protein (40K) precursor.  
 GN OMPL.  
 OS Fusobacterium nucleatum.  
 OC Bacteria; Fusobacteria; Fusobacteriales; Fusobacteriaceae;  
 OC Fusobacterium.  
 OX NCBI\_TaxID=851;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Fev1;  
 RX MEDLINE=94010332; PubMed=8406032;  
 RA Bolstad A.I., Jensen H.B.;  
 RT "Complete sequence of ompl, the structural gene encoding the 40-kDa  
 RT outer membrane protein of Fusobacterium nucleatum strain Fev1.";  
 RL Gene 132:107-112(1993).  
 DR EMBL; X66735; CAA47273.1; -.  
 KW Signal.  
 FT SIGNAL 1 20 POTENTIAL.  
 FT CHAIN 21 368 OUTER MEMBRANE PROTEIN (40K).  
 SQ SEQUENCE 368 AA; 41918 MW; 13E15C1E2E3DEE82 CRC64;  
 Query Match 90.0%; Score 27; DB 2; Length 368;  
 Best Local Similarity 83.3%; Pred. No. 3.8e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SVDVEY 6  
 Db 59 SVDVQY 64  
 RESULT 45  
 Q47903 PRELIMINARY; PRT; 368 AA.  
 ID Q47903  
 AC Q47903;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE Porin precursor.  
 GN FOMA.  
 OS Fusobacterium nucleatum (subsp. nucleatum).  
 OC Bacteria; Fusobacteria; Fusobacteriales; Fusobacteriaceae;  
 OC Fusobacterium.  
 OX NCBI\_TaxID=76856;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ATCC 25586;  
 RX MEDLINE=94316187; PubMed=8041356;  
 RA Bolstad A.I., Tommassen J., Jensen H.B.;  
 RT "Sequence variability of the 40-kDa outer membrane proteins of

RT Fusobacterium nucleatum strains and a model for the topology of the  
 RT proteins.";  
 RL Mol. Gen. Genet. 244:104-110(1994).  
 DR EMBL; X72582; CAA51172.1; -.  
 KW Signal.  
 FT SIGNAL 1 20 POTENTIAL.  
 FT CHAIN 21 368 PORIN.  
 SQ SEQUENCE 368 AA; 42373 MW; 3B20A95BBE66D23C CRC64;  
 Query Match 90.0%; Score 27; DB 2; Length 368;  
 Best Local Similarity 83.3%; Pred. No. 3.8e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SVDVEY 6  
 Db 59 SVDVQY 64  
 RESULT 46  
 Q8RHY1 PRELIMINARY; PRT; 368 AA.  
 ID Q8RHY1  
 AC Q8RHY1;  
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE Major outer membrane protein.  
 GN FNI859.  
 OS Fusobacterium nucleatum (subsp. nucleatum).  
 OC Bacteria; Fusobacteria; Fusobacteriales; Fusobacteriaceae;  
 OC Fusobacterium.  
 OX NCBI\_TaxID=76856;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ATCC 25586;  
 RX MEDLINE=21886394; PubMed=11889109;  
 RA Kapatal V., Anderson I., Ivanova N., Reznik G., Los T., Lykidis A.,  
 RA Bhattacharya A., Bartman A., Gardner W., Grechkin G., Zhu L.,  
 RA Vasileva O., Chu L., Kogan Y., Chaga O., Goltzman E., Bernal A.,  
 RA Larsen N., D'Souza M., Walunas T., Pusch G., Haselkorn R.,  
 RA Fongstein M., Kyripides N., Overbeek R.;  
 RT "Genome sequence and analysis of the oral bacterium Fusobacterium  
 RT nucleatum strain ATCC 25586.";  
 RL J. Bacteriol. 184:2005-2018(2002).  
 DR EMBL; AE010488; AAL93958.1; -.  
 KW Complete proteome.  
 SQ SEQUENCE 368 AA; 42373 MW; 131624D9EB017626 CRC64;  
 Query Match 90.0%; Score 27; DB 16; Length 368;  
 Best Local Similarity 83.3%; Pred. No. 3.8e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SVDVEY 6  
 Db 59 SVDVQY 64  
 RESULT 47  
 Q47905 PRELIMINARY; PRT; 370 AA.  
 ID Q47905  
 AC Q47905;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE Porin precursor.  
 GN FOMA.  
 OS Fusobacterium nucleatum (subsp. polymorphum).  
 OC Bacteria; Fusobacteria; Fusobacteriales; Fusobacteriaceae;  
 OC Fusobacterium.  
 OX NCBI\_TaxID=76857;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ATCC 10953;  
 RX MEDLINE=94316187; PubMed=8041356;

```

RA Bolstad A.I., Tomassen J., Jensen H.B.;
RT "Sequence variability of the 40-kDa outer membrane proteins of
RT Fusobacterium nucleatum strains and a model for the topology of the
RT proteins.";
RL Mol. Gen. Genet. 244:104-110(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 10953;
RA Bolstad A.I.;
RL Submitted (MAR-1993) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 10953;
RA Bolstad A.I.;
RL Submitted (AUG-1994) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 10953;
RA Bolstad A.I.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 10953;
RA Jensen H.B.;
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; X72583; CAA51173.2; -.
KW SIGNAL.
FT SIGNAL 1 20 POTENTIAL.
FT CHAIN 21 370 PORIN.
SQ SEQUENCE 370 AA; 42241 MW; 7816111E6F206012F CRC64;

Query Match 90.0%; Score 27; DB 2; Length 370;
Best Local Similarity 83.3%; Pred. No. 3.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVEY 6
DB 59 SVDVQY 64

RESULT 48
Q47913 PRELIMINARY; PRT; 372 AA.
AC Q47913;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Major outer membrane 40kDa protein FomA.
GN FOM.
OS Fusobacterium periodonticum.
OC Bacteria; Fusobacteria; Fusobacteriales; Fusobacteriaceae;
OC Fusobacterium.
OX NCBI_TaxID=860;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC;
RX MEDLINE=96179239; PubMed=8596666;
RA Bolstad A.I., Hogg B.T., Jensen H.B.;
RT "Molecular characterization of a 40-kDa outer membrane protein, FomA,
RT of Fusobacterium periodonticum and comparison with Fusobacterium
RT nucleatum.";
RL Oral Microbiol. Immunol. 10:257-264(1995).
DR EMBL; X82023; CAA57547.1; -.
FT CHAIN 21 372 MAJOR OUTER MEMBRANE 40KDA PROTEIN FOM.
SQ SEQUENCE 372 AA; 42265 MW; 5DFC806A50D48F56 CRC64;

Query Match 90.0%; Score 27; DB 2; Length 372;
Best Local Similarity 83.3%; Pred. No. 3.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVEY 6
DB 59 SVDVQY 64

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RESULT 49
Q8F8E1 PRELIMINARY; PRT; 374 AA.
AC Q8F8E1;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Outer membrane lipoprotein lipL41.
GN LIP41 OR LA0616.
OS Leptospira interrogans.
OC Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.
OX NCBI_TaxID=173;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=56601 / Serogroup Icterohaemorrhagiae / Seroovar lai;
RA Ren S.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB011248; AAN47815.1; -.
KW Lipoprotein; Complete proteome.
SQ SEQUENCE 374 AA; 41070 MW; 3A3F9EB94BFDC1A0 CRC64;

Query Match 90.0%; Score 27; DB 16; Length 374;
Best Local Similarity 83.3%; Pred. No. 3.9e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVEY 6
DB 42 TVDVEY 47

RESULT 50
Q8X4C8 PRELIMINARY; PRT; 375 AA.
AC Q8X4C8;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Putative tail component encoded by cryptic prophage CP-933M,
DE partial.
GN Z1382.
OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=83334;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / EDL933 / ATCC 700927;
RX MEDLINE=21074935; PubMed=11208551;
RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamoudis K.,
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blattner F.R.;
RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
RL Nature 409:529-533(2001).
DR EMBL; AE005290; AAG55515.1; -.
DR InterPro; IPR000087; Collagen.
DR Pfam; PF01391; Collagen; 2.
KW Complete proteome.
SQ SEQUENCE 375 AA; 37493 MW; 6BC3CF5F93757C62 CRC64;

Query Match 90.0%; Score 27; DB 16; Length 375;
Best Local Similarity 83.3%; Pred. No. 3.9e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVEY 6
DB 52 SMDVEY 57

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Search completed: January 20, 2004, 13:57:40  
Job time : 39 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 20, 2004, 13:56:22 ; Search time 24 Seconds  
(without alignments)  
18.415 Million cell updates/sec

Title:  
Perfect score: 30  
Sequence: 1 SVDVEY 6

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 354356 seqs, 73659510 residues

Total number of hits satisfying chosen parameters: 354356

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 75 summaries

Database : Pending Patents AA New:  
1: /cgn2\_6/ptodata/1/paa/PCT\_NEW\_COMB.pep.\*  
2: /cgn2\_6/ptodata/1/paa/USC6\_NEW\_COMB.pep.\*  
3: /cgn2\_6/ptodata/1/paa/USC7\_NEW\_COMB.pep.\*  
4: /cgn2\_6/ptodata/1/paa/USC8\_NEW\_COMB.pep.\*  
5: /cgn2\_6/ptodata/1/paa/USC9\_NEW\_COMB.pep.\*  
6: /cgn2\_6/ptodata/1/paa/US10\_NEW\_COMB.pep.\*  
7: /cgn2\_6/ptodata/1/paa/US60\_NEW\_COMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	ID	Description
1	30	100.0	440	6	US-10-415-182A-8298	Sequence 8298, Ap
2	29	96.7	520	5	US-09-614-150A-25695	Sequence 25695, A
3	29	96.7	615	6	US-10-679-063-26860	Sequence 26860, A
4	29	96.7	1190	5	US-09-614-150A-3243	Sequence 3243, Ap
5	27	90.0	17	6	US-10-474-601-11	Sequence 11, Appl
6	27	90.0	268	6	US-10-425-114A-59564	Sequence 59564, A
7	27	90.0	515	5	US-09-614-150A-25056	Sequence 25056, A
8	27	90.0	562	7	US-60-483-317-62	Sequence 62, Appl
9	27	90.0	562	7	US-60-483-317-60	Sequence 60, Appl
10	27	90.0	858	7	US-60-482-992-14	Sequence 14, Appl
11	26	86.7	140	6	US-10-425-114A-54666	Sequence 54666, A
12	26	86.7	158	6	US-10-679-063-1932	Sequence 1932, Ap
13	26	86.7	160	6	US-10-679-063-25025	Sequence 25025, A
14	26	86.7	164	6	US-10-679-063-1285	Sequence 1285, Ap
15	26	86.7	164	6	US-10-679-063-25896	Sequence 25896, A
16	26	86.7	166	6	US-10-679-063-15897	Sequence 15897, A
17	26	86.7	178	6	US-10-415-182A-3474	Sequence 3474, Ap
18	26	86.7	201	1	PCT-US03-40618-7251	Sequence 7251, Ap
19	26	86.7	201	6	US-10-741-849-7251	Sequence 7251, Ap
20	26	86.7	212	7	US-60-495-114-1576	Sequence 1576, Ap
21	26	86.7	244	6	US-10-389-647-692	Sequence 692, Appl
22	26	86.7	282	6	US-10-701-283-43	Sequence 43, Appl
23	26	86.7	284	6	US-10-701-283-42	Sequence 42, Appl
24	26	86.7	285	6	US-10-701-283-12	Sequence 12, Appl
25	26	86.7	303	5	US-09-614-150A-36165	Sequence 36165, A
26	26	86.7	316	5	US-09-897-516A-6610	Sequence 6610, Ap

ALIGNMENTS

RESULT 1

US-10-415-182A-8298  
; Sequence 8298, Application US/10415182A  
; GENERAL INFORMATION:  
; APPLICANT: Telford, John  
; TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B  
; FILE REFERENCE:  
; CURRENT FILING DATE: 2003-12-09  
; PRIOR APPLICATION NUMBER: GB-0026333.5  
; PRIOR FILING DATE: 2000-10-27  
; PRIOR APPLICATION NUMBER: GB-0028727.6  
; PRIOR FILING DATE: 2000-11-24  
; PRIOR APPLICATION NUMBER: GB-0105640.7  
; PRIOR FILING DATE: 2001-03-07  
; NUMBER OF SEQ ID NOS: 12024  
; SOFTWARE: SeqWin99, version 1.02  
; SEQ ID NO 8298  
; LENGTH: 440

27	86.7	337	6	US-10-425-114A-40092	Sequence 40092, A
28	86.7	341	6	US-10-425-114A-64094	Sequence 64094, A
29	86.7	366	6	US-10-739-930-10318	Sequence 10318, A
30	86.7	408	6	US-10-415-182A-9892	Sequence 9892, Ap
31	86.7	420	6	US-10-415-182A-2698	Sequence 2698, Ap
32	86.7	428	6	US-10-473-040-683	Sequence 683, App
33	86.7	442	7	US-60-479-962-447	Sequence 447, App
34	86.7	455	6	US-10-739-930-5786	Sequence 5786, Ap
35	86.7	460	6	US-10-679-063-16687	Sequence 16687, A
36	86.7	532	6	US-10-679-063-2191	Sequence 2191, Ap
37	86.7	572	6	US-10-472-928-3056	Sequence 3056, Ap
38	86.7	597	6	US-10-679-063-2707	Sequence 2707, Ap
39	86.7	606	6	US-10-451-168-56	Sequence 56, Appl
40	86.7	606	6	US-10-451-168-57	Sequence 57, Appl
41	86.7	615	5	US-09-614-150A-18810	Sequence 18810, A
42	86.7	633	5	US-09-614-150A-3981	Sequence 3981, Ap
43	86.7	673	7	US-60-495-589-168	Sequence 168, App
44	86.7	676	6	US-10-418-861B-42	Sequence 42, Appl
45	86.7	883	6	US-10-475-292-167	Sequence 167, App
46	86.7	891	5	US-09-581-286A-442	Sequence 442, App
47	86.7	899	5	US-09-581-286A-316	Sequence 316, App
48	86.7	1082	5	US-09-614-150A-16857	Sequence 16857, A
49	86.7	1137	5	US-09-614-150A-18237	Sequence 18237, A
50	83.3	50	6	US-10-472-928-972	Sequence 972, App
51	83.3	73	6	US-10-425-114A-54656	Sequence 54656, A
52	83.3	152	6	US-10-679-063-24273	Sequence 24273, A
53	83.3	155	6	US-10-679-063-9848	Sequence 9848, Ap
54	83.3	156	6	US-10-679-063-9601	Sequence 9601, Ap
55	83.3	164	6	US-10-679-063-19431	Sequence 19431, A
56	83.3	165	6	US-10-679-063-19378	Sequence 19378, A
57	83.3	240	6	US-10-425-114A-45585	Sequence 45585, A
58	83.3	248	6	US-10-425-114A-37285	Sequence 37285, A
59	83.3	269	6	US-10-472-260-160	Sequence 160, App
60	83.3	270	6	US-10-275-026A-142	Sequence 142, App
61	83.3	271	6	US-10-275-026A-44	Sequence 44, Appl
62	83.3	282	6	US-10-425-114A-44434	Sequence 44434, A
63	83.3	299	6	US-10-425-114A-51168	Sequence 51168, A
64	83.3	325	6	US-10-425-114A-53847	Sequence 53847, A
65	83.3	329	6	US-10-679-063-17455	Sequence 17455, A
66	83.3	336	5	US-09-897-516A-6690	Sequence 6690, Ap
67	83.3	379	6	US-10-425-114A-53742	Sequence 53742, A
68	83.3	409	5	US-09-614-150A-25236	Sequence 25236, A
69	83.3	410	1	PCT-US03-30770-15	Sequence 15, Appl
70	83.3	421	6	US-10-425-114A-64896	Sequence 64896, A
71	83.3	421	6	US-10-425-114A-72361	Sequence 72361, A
72	83.3	424	6	US-10-679-063-859	Sequence 859, App
73	83.3	424	6	US-10-679-063-3844	Sequence 3844, Ap
74	83.3	451	5	US-09-614-150A-40437	Sequence 40437, A
75	83.3	466	6	US-10-415-182A-6540	Sequence 6540, Ap

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; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-10-415-182A-8298

Query Match      100.0%; Score 30; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SVDVEY 6
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Db      183 SVDVEY 188

RESULT 2
US-09-614-150A-25695
; Sequence 25695, Application US/09614150A
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; TITLE OF INVENTION: DROSOPHILA GENES.
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/09/614,150A
; CURRENT FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25695
; LENGTH: 520
; TYPE: PRT
; ORGANISM: DROSOPHILA
US-09-614-150A-25695

Query Match      96.7%; Score 29; DB 5; Length 520;
Best Local Similarity 83.3%; Pred. No. 1.1e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 SVDVEY 6
      |||||
Db      182 SVDVEY 187

RESULT 3
US-10-679-063-26860
; Sequence 26860, Application US/10679063
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52054)B
; CURRENT APPLICATION NUMBER: US/10/679,063
; CURRENT FILING DATE: 2003-10-02
; PRIOR APPLICATION NUMBER: 60/415,758
; PRIOR FILING DATE: 2002-10-02
; NUMBER OF SEQ ID NOS: 27373
; SEQ ID NO 26860
; LENGTH: 615
; TYPE: PRT
; ORGANISM: DROSOPHILA
US-10-679-063-26860

Query Match      96.7%; Score 29; DB 5; Length 1190;
Best Local Similarity 83.3%; Pred. No. 1.5e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 SVDVEY 6
      |||||
Db      682 SVDIEY 687

RESULT 4
US-09-614-150A-3243
; Sequence 3243, Application US/09614150A
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; TITLE OF INVENTION: DROSOPHILA GENES.
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/09/614,150A
; CURRENT FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3243
; LENGTH: 1190
; TYPE: PRT
; ORGANISM: DROSOPHILA
US-09-614-150A-3243

Query Match      96.7%; Score 29; DB 5; Length 1190;
Best Local Similarity 83.3%; Pred. No. 1.5e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 SVDVEY 6
      |||||
Db      682 SVDIEY 687

RESULT 5
US-10-474-601-11
; Sequence 11, Application US/10474601
; GENERAL INFORMATION:
; APPLICANT: Friedrich, Thomas
; APPLICANT: Zimmerman, Norbert
; APPLICANT: Sturmer, Rainer
; TITLE OF INVENTION: Reaction of (di)amines in the presence
; TITLE OF INVENTION: of a lysin oxidase and of a reducing agent
; FILE REFERENCE: BGI-156US
; CURRENT APPLICATION NUMBER: US/10/474,601
; CURRENT FILING DATE: 2003-10-09
; PRIOR APPLICATION NUMBER: PCT/EP02/03873
; PRIOR FILING DATE: 2003-10-09
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
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; SEQ ID NO 11
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Pichia pastoris
US-10-474-601-11

Query Match          90.0%; Score 27; DB 6; Length 17;
Best Local Similarity 83.3%; Pred. No. 6.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVEY 6
   :|||||
Db 1 NVDVEY 6

RESULT 6
US-10-425-114A-59564
; Sequence 59564, Application US/10425114A
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114A
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 59564
; LENGTH: 268
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3587-216-D2_FLI.pep
US-10-425-114A-59564

Query Match          90.0%; Score 27; DB 6; Length 268;
Best Local Similarity 83.3%; Pred. No. 1.6e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVEY 6
   :|||||
Db 68 TVDVEY 73

RESULT 7
US-09-614-150A-25056
; Sequence 25056, Application US/09614150A
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; TITLE OF INVENTION: DROSOPHILA GENES.
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/09/614,150A
; CURRENT FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831

; SEQ ID NO 11
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Pichia pastoris
US-10-474-601-11

; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25056
; LENGTH: 515
; TYPE: PRT
; ORGANISM: DROSOPHILA
US-09-614-150A-25056

Query Match          90.0%; Score 27; DB 5; Length 515;
Best Local Similarity 83.3%; Pred. No. 2.1e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVEY 6
   :|||||
Db 451 SVDVEY 456

RESULT 8
US-60-483-917-62
; Sequence 62, Application US/60483917
; GENERAL INFORMATION:
; APPLICANT: Gan, Li
; APPLICANT: Shivak, David
; APPLICANT: Chin, Daniel J
; APPLICANT: von Schack, David
; APPLICANT: Uffer, Roman
; APPLICANT: Gonzalez-Zulueta, Mirella
; TITLE OF INVENTION: NUCLEIC ACIDS ASSOCIATED WITH NEURODEGENERATIVE DISORDERS
; FILE REFERENCE: 00208.0013.PZUS00
; CURRENT APPLICATION NUMBER: US/60/483,917
; CURRENT FILING DATE: 2003-06-30
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 62
; LENGTH: 562
; TYPE: PRT
; ORGANISM: Mus musculus
US-60-483-917-62

Query Match          90.0%; Score 27; DB 7; Length 562;
Best Local Similarity 83.3%; Pred. No. 2.1e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVEY 6
   :|||||
Db 273 SLDVEY 278

RESULT 9
US-60-483-917-60
; Sequence 60, Application US/60483917
; GENERAL INFORMATION:
; APPLICANT: Gan, Li
; APPLICANT: Shivak, David
; APPLICANT: Chin, Daniel J
; APPLICANT: von Schack, David
; APPLICANT: Uffer, Roman
; APPLICANT: Gonzalez-Zulueta, Mirella
; TITLE OF INVENTION: NUCLEIC ACIDS ASSOCIATED WITH NEURODEGENERATIVE DISORDERS
; FILE REFERENCE: 00208.0013.PZUS00
; CURRENT APPLICATION NUMBER: US/60/483,917
; CURRENT FILING DATE: 2003-06-30
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 60
; LENGTH: 563
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-60-483-917-60

```

Query Match  
Best Local Similarity 90.0%; Score 27; DB 7; Length 563;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVEY 6  
Db 274 SLDVEY 279

RESULT 10  
US-60-482-992-14  
; Sequence 14, Application US/60482992  
; GENERAL INFORMATION:  
; APPLICANT: Li, Xia  
; APPLICANT: Li, Weihua  
; APPLICANT: Reed, Danielle  
; APPLICANT: Bachmanov, Alexander  
; APPLICANT: Brand, Joseph  
; TITLE OF INVENTION: Taste Receptor Of The TIR Family From Domestic Cat  
; FILE REFERENCE: MON3042  
; CURRENT APPLICATION NUMBER: US/60/482,992  
; CURRENT FILING DATE: 2003-06-27  
; NUMBER OF SEQ ID NOS: 58  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 14  
; LENGTH: 858  
; TYPE: PRT  
; ORGANISM: Rattus rattus  
US-60-482-992-14

Query Match  
Best Local Similarity 90.0%; Score 27; DB 7; Length 858;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVEY 6  
Db 456 SVDVEY 461

RESULT 11  
US-10-425-114A-54666  
; Sequence 54666, Application US/10425114A  
; GENERAL INFORMATION:  
; APPLICANT: Liu, Jingdong  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Screen, Steven E.  
; APPLICANT: Tabaska, Jack E.  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(53313)B  
; CURRENT APPLICATION NUMBER: US/10/425,114A  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 73128  
; SEQ ID NO 54666  
; LENGTH: 140  
; TYPE: PRT  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: UC-ZMFLMO17169G05\_F11.pep  
US-10-425-114A-54666

Query Match  
Best Local Similarity 86.7%; Score 26; DB 6; Length 140;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDVEY 6  
Db 84 VDVEY 88

RESULT 12

US-10-679-063-1932  
; Sequence 1932, Application US/10679063  
; GENERAL INFORMATION:  
; APPLICANT: Edgerton, Michael D  
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES  
; FILE REFERENCE: 38-15(52054)B  
; CURRENT APPLICATION NUMBER: US/10/679,063  
; CURRENT FILING DATE: 2003-10-02  
; PRIOR APPLICATION NUMBER: 60/415,758  
; PRIOR FILING DATE: 2002-10-02  
; NUMBER OF SEQ ID NOS: 27373  
; SEQ ID NO 1932  
; LENGTH: 158  
; TYPE: PRT  
; ORGANISM: Glycine max  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (1)..(158)  
; OTHER INFORMATION: unsure at all Xaa locations  
US-10-679-063-1932

Query Match  
Best Local Similarity 86.7%; Score 26; DB 6; Length 158;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SVDVEY 6  
Db 3 SADVEY 8

RESULT 13  
US-10-679-063-25025  
; Sequence 25025, Application US/10679063  
; GENERAL INFORMATION:  
; APPLICANT: Edgerton, Michael D  
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES  
; FILE REFERENCE: 38-15(52054)B  
; CURRENT APPLICATION NUMBER: US/10/679,063  
; CURRENT FILING DATE: 2003-10-02  
; PRIOR APPLICATION NUMBER: 60/415,758  
; PRIOR FILING DATE: 2002-10-02  
; NUMBER OF SEQ ID NOS: 27373  
; SEQ ID NO 25025  
; LENGTH: 160  
; TYPE: PRT  
; ORGANISM: Glycine max  
US-10-679-063-25025

Query Match  
Best Local Similarity 86.7%; Score 26; DB 6; Length 160;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SVDVEY 6  
Db 3 SADVEY 8

RESULT 14  
US-10-679-063-1285  
; Sequence 1285, Application US/10679063  
; GENERAL INFORMATION:  
; APPLICANT: Edgerton, Michael D  
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES  
; FILE REFERENCE: 38-15(52054)B  
; CURRENT APPLICATION NUMBER: US/10/679,063  
; CURRENT FILING DATE: 2003-10-02  
; PRIOR APPLICATION NUMBER: 60/415,758  
; PRIOR FILING DATE: 2002-10-02  
; NUMBER OF SEQ ID NOS: 27373  
; SEQ ID NO 1285  
; LENGTH: 164  
; TYPE: PRT  
; ORGANISM: Glycine max



```

;
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)-(164)
; OTHER INFORMATION: unsure at all Xaa locations
US-10-679-063-1285

Query Match      86.7%; Score 26; DB 6; Length 164;
Best Local Similarity 83.3%; Pred. No. 1.9e+03;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SVDVEY 6
   | ||||
Db 3 SADVEY 8

RESULT 15
US-10-679-063-25896
; Sequence 25896, Application US/10679063
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52054)B
; CURRENT APPLICATION NUMBER: US/10/679,063
; CURRENT FILING DATE: 2003-10-02
; PRIOR APPLICATION NUMBER: 60/415,758
; PRIOR FILING DATE: 2002-10-02
; NUMBER OF SEQ ID NOS: 27373
; SEQ ID NO 25896
; LENGTH: 164
; TYPE: PRT
; ORGANISM: Catharanthus roseus
US-10-679-063-25896

Query Match      86.7%; Score 26; DB 6; Length 164;
Best Local Similarity 83.3%; Pred. No. 1.9e+03;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SVDVEY 6
   | ||||
Db 3 SADVEY 8

RESULT 16
US-10-679-063-15897
; Sequence 15897, Application US/10679063
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52054)B
; CURRENT APPLICATION NUMBER: US/10/679,063
; CURRENT FILING DATE: 2003-10-02
; PRIOR APPLICATION NUMBER: 60/415,758
; PRIOR FILING DATE: 2002-10-02
; NUMBER OF SEQ ID NOS: 27373
; SEQ ID NO 15897
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Pelargonium x hortorum
US-10-679-063-15897

Query Match      86.7%; Score 26; DB 6; Length 166;
Best Local Similarity 83.3%; Pred. No. 1.9e+03;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SVDVEY 6
   | ||||
Db 3 SADVEY 8

RESULT 17
US-10-415-182A-3474
; Sequence 3474, Application US/10415182A
; GENERAL INFORMATION:
; APPLICANT: Telford, John
; TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/415,182A
; CURRENT FILING DATE: 2003-12-09
; PRIOR APPLICATION NUMBER: GB-0026333.5
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: GB-0028727.6
; PRIOR FILING DATE: 2000-11-24
; PRIOR APPLICATION NUMBER: GB-0105640.7
; PRIOR FILING DATE: 2001-03-07
; NUMBER OF SEQ ID NOS: 12024
; SOFTWARE: Seqwin99, version 1.02
; SEQ ID NO 3474
; LENGTH: 178
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-10-415-182A-3474

Query Match      86.7%; Score 26; DB 6; Length 178;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDVVEY 6
   | ||||
Db 45 VDVVEY 49

RESULT 18
PCT-US03-40618-7251
; Sequence 7251, Application PC/TUS0340618
; GENERAL INFORMATION:
; APPLICANT: Elittra Pharmaceuticals, Inc.
; APPLICANT: Elittra Canada Limited
; TITLE OF INVENTION: Nucleic Acids Encoding Anti-fungal Drug Targets and Methods of
; TITLE OF INVENTION: Use
; FILE REFERENCE: 10182-023-228
; CURRENT APPLICATION NUMBER: PCT/US03/40618
; CURRENT FILING DATE: 2003-12-19
; PRIOR APPLICATION NUMBER: US 60/434,832
; PRIOR FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 8000
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7251
; LENGTH: 201
; TYPE: PRT
; ORGANISM: Candida albicans
PCT-US03-40618-7251

Query Match      86.7%; Score 26; DB 1; Length 201;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDVVEY 6
   | ||||
Db 192 VDVVEY 196

RESULT 19
US-10-741-849-7251
; Sequence 7251, Application US/10741849
; GENERAL INFORMATION:
; APPLICANT: Roemer, Terry
; APPLICANT: Jiang, Bo
; APPLICANT: Boone, Charles
; APPLICANT: Bussey, Howard
; TITLE OF INVENTION: Nucleic Acids Encoding Anti-fungal Drug Targets and Methods of
; TITLE OF INVENTION: Use
; FILE REFERENCE: 10182-023-999
; CURRENT APPLICATION NUMBER: US/10/741,849
; CURRENT FILING DATE: 2003-12-19
; PRIOR APPLICATION NUMBER: US 60/434,832
; PRIOR FILING DATE: 2002-12-19
```

; NUMBER OF SEQ ID NOS: 8000  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 7251  
; LENGTH: 201  
; TYPE: PRT  
; ORGANISM: Candida albicans  
US-10-741-849-7251

Query Match 86.7%; Score 26; DB 6; Length 201;  
Best Local Similarity 100.0%; Pred. No. 2e+03;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 2 VDVEY 6  
Db 192 VDVEY 196

RESULT 20  
US-60-495-114-1576  
; Sequence 1576, Application US/60495114  
; GENERAL INFORMATION:  
; APPLICANT: CARIGILL, Michele  
; TITLE OF INVENTION: POLYMORPHISMS IN NUCLEIC ACID MOLECULES  
; TITLE OF INVENTION: ENCODING HUMAN PROTEASE PROTEINS, METHODS OF DETECTION AND  
; TITLE OF INVENTION: USES THEREOF  
; FILE REFERENCE: C1001480  
; CURRENT APPLICATION NUMBER: US/60/495,114  
; CURRENT FILING DATE: 2003-08-15  
; NUMBER OF SEQ ID NOS: 91238  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1576  
; LENGTH: 212  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-60-495-114-1576

Query Match 86.7%; Score 26; DB 7; Length 212;  
Best Local Similarity 83.3%; Pred. No. 2e+03;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 SVDVEY 6  
Db 139 SVEVEY 144

RESULT 21  
US-10-389-647-692  
; Sequence 692, Application US/10389647  
; GENERAL INFORMATION:  
; APPLICANT: GREENBERG, E. Peter  
; APPLICANT: SCHUSTER, Martin  
; APPLICANT: LOSTROH, Candi  
; TITLE OF INVENTION: QUORUM SENSING SIGNALING IN BACTERIA  
; FILE REFERENCE: U12-038CP  
; CURRENT APPLICATION NUMBER: US/10/389,647  
; CURRENT FILING DATE: 2003-03-14  
; PRIOR APPLICATION NUMBER: 09/653730  
; PRIOR FILING DATE: 2000-09-01  
; PRIOR APPLICATION NUMBER: 60/153022  
; PRIOR FILING DATE: 1999-09-03  
; NUMBER OF SEQ ID NOS: 710  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 692  
; LENGTH: 244  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-10-389-647-692

Query Match 86.7%; Score 26; DB 6; Length 244;  
Best Local Similarity 83.3%; Pred. No. 2.1e+03;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 SVDVEY 6

Db 215 SADVEY 220

RESULT 22  
US-10-701-283-43  
; Sequence 43, Application US/10701283  
; GENERAL INFORMATION:  
; APPLICANT: Spaderna, Steven K  
; APPLICANT: Quinn, Kerry E.  
; APPLICANT: Shimkets, Richard A.  
; APPLICANT: Muralidhara, Padigaru  
; APPLICANT: Spytek, Kimberly A.  
; TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same  
; FILE REFERENCE: 15966-620 CIP  
; CURRENT APPLICATION NUMBER: US/10/701,283  
; CURRENT FILING DATE: 2003-11-03  
; PRIOR APPLICATION NUMBER: US/09/737,149  
; PRIOR FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: 60/170,564  
; PRIOR FILING DATE: 1999-12-14  
; PRIOR APPLICATION NUMBER: 60/173,165  
; PRIOR FILING DATE: 1999-12-27  
; PRIOR APPLICATION NUMBER: 60/173,362  
; PRIOR FILING DATE: 1999-12-27  
; PRIOR APPLICATION NUMBER: 60/173,544  
; PRIOR FILING DATE: 1999-12-29  
; PRIOR APPLICATION NUMBER: 60/174,404  
; PRIOR FILING DATE: 2000-01-04  
; PRIOR APPLICATION NUMBER: 60/174,962  
; PRIOR FILING DATE: 2000-01-07  
; PRIOR APPLICATION NUMBER: 60/223,929  
; PRIOR FILING DATE: 2000-08-09  
; NUMBER OF SEQ ID NOS: 49  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 43  
; LENGTH: 282  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Consensus Sequence  
; NAME/KEY: VARIANT  
; LOCATION: (1)..(282)  
; OTHER INFORMATION: Where X is a residue at which the query and  
; OTHER INFORMATION: subject sequences are not identical.  
US-10-701-283-43

Query Match 86.7%; Score 26; DB 6; Length 282;  
Best Local Similarity 66.7%; Pred. No. 2.2e+03;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 SVDVEY 6  
Db 2 AVDIEY 7

RESULT 23  
US-10-701-283-42  
; Sequence 42, Application US/10701283  
; GENERAL INFORMATION:  
; APPLICANT: Spaderna, Steven K  
; APPLICANT: Quinn, Kerry E.  
; APPLICANT: Shimkets, Richard A.  
; APPLICANT: Muralidhara, Padigaru  
; APPLICANT: Spytek, Kimberly A.  
; TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same  
; FILE REFERENCE: 15966-620 CIP  
; CURRENT APPLICATION NUMBER: US/10/701,283  
; CURRENT FILING DATE: 2003-11-03  
; PRIOR APPLICATION NUMBER: US/09/737,149  
; PRIOR FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: 60/170,564

;; PRIOR FILING DATE: 1999-12-14  
;; PRIOR APPLICATION NUMBER: 60/173,165  
;; PRIOR FILING DATE: 1999-12-27  
;; PRIOR APPLICATION NUMBER: 60/173,362  
;; PRIOR FILING DATE: 1999-12-27  
;; PRIOR APPLICATION NUMBER: 60/173,544  
;; PRIOR FILING DATE: 1999-12-29  
;; PRIOR APPLICATION NUMBER: 60/174,404  
;; PRIOR FILING DATE: 2000-01-04  
;; PRIOR APPLICATION NUMBER: 60/174,962  
;; PRIOR FILING DATE: 2000-01-07  
;; PRIOR APPLICATION NUMBER: 60/223,929  
;; PRIOR FILING DATE: 2000-08-09  
;; NUMBER OF SEQ ID NOS: 49  
;; SOFTWARE: PatentIn Ver. 2.0  
;; SEQ ID NO 42  
;; LENGTH: 284  
;; TYPE: PRT  
;; ORGANISM: Rattus norvegicus  
US-10-701-283-42

Query Match 86.7%; Score 26; DB 6; Length 284;  
Best Local Similarity 66.7%; Pred. No. 2.3e+03;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVDVEY 6  
Db 2 AVDIEY 7

RESULT 24  
US-10-701-283-12  
;; Sequence 12, Application US/10701283  
;; GENERAL INFORMATION:  
;; APPLICANT: Spaderna, Steven K  
;; APPLICANT: Quinn, Kerry E.  
;; APPLICANT: Shimkets, Richard A.  
;; APPLICANT: Muralidhara, Padigaru  
;; APPLICANT: Spytek, Kimberly A.  
;; TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same  
;; FILE REFERENCE: 15966-620 CIP  
;; CURRENT APPLICATION NUMBER: US/10701,283  
;; CURRENT FILING DATE: 2003-11-03  
;; PRIOR APPLICATION NUMBER: US/09/737,149  
;; PRIOR FILING DATE: 2001-06-15  
;; PRIOR APPLICATION NUMBER: 60/170,564  
;; PRIOR FILING DATE: 1999-12-14  
;; PRIOR APPLICATION NUMBER: 60/173,165  
;; PRIOR FILING DATE: 1999-12-27  
;; PRIOR APPLICATION NUMBER: 60/173,362  
;; PRIOR FILING DATE: 1999-12-27  
;; PRIOR APPLICATION NUMBER: 60/173,544  
;; PRIOR FILING DATE: 1999-12-29  
;; PRIOR APPLICATION NUMBER: 60/174,404  
;; PRIOR FILING DATE: 2000-01-04  
;; PRIOR APPLICATION NUMBER: 60/174,962  
;; PRIOR FILING DATE: 2000-01-07  
;; PRIOR APPLICATION NUMBER: 60/223,929  
;; PRIOR FILING DATE: 2000-08-09  
;; NUMBER OF SEQ ID NOS: 49  
;; SOFTWARE: PatentIn Ver. 2.0  
;; SEQ ID NO 12  
;; LENGTH: 285  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
US-10-701-283-12

Query Match 86.7%; Score 26; DB 6; Length 285;  
Best Local Similarity 66.7%; Pred. No. 2.3e+03;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVDVEY 6  
Db 2 AVDIEY 7

Db 3 AVDIEY 8  
RESULT 25  
US-09-614-150A-36165

;; Sequence 36165, Application US/09614150A  
;; GENERAL INFORMATION:  
;; APPLICANT: Venter, J. Craig  
;; APPLICANT: et al.  
;; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID  
;; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE  
;; TITLE OF INVENTION: DROSOPHILA GENES.  
;; FILE REFERENCE: CL000728  
;; CURRENT APPLICATION NUMBER: US/09/614,150A  
;; CURRENT FILING DATE: 2000-07-11  
;; PRIOR APPLICATION NUMBER: 60/157,832  
;; PRIOR FILING DATE: 1999-10-05  
;; PRIOR APPLICATION NUMBER: 60/160,191  
;; PRIOR FILING DATE: 1999-10-19  
;; PRIOR APPLICATION NUMBER: 60/161,932  
;; PRIOR FILING DATE: 1999-10-28  
;; PRIOR APPLICATION NUMBER: 60/164,769  
;; PRIOR FILING DATE: 1999-11-12  
;; PRIOR APPLICATION NUMBER: 60/173,383  
;; PRIOR FILING DATE: 1999-12-28  
;; PRIOR APPLICATION NUMBER: 60/175,693  
;; PRIOR FILING DATE: 2000-01-12  
;; PRIOR APPLICATION NUMBER: 60/184,831  
;; PRIOR FILING DATE: 2000-02-24  
;; PRIOR APPLICATION NUMBER: 60/191,637  
;; PRIOR FILING DATE: 2000-03-23  
;; NUMBER OF SEQ ID NOS: 43008  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 36165  
;; LENGTH: 303  
;; TYPE: PRT  
;; ORGANISM: DROSOPHILA  
US-09-614-150A-36165

Query Match 86.7%; Score 26; DB 5; Length 303;  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VDVVEY 6  
Db 262 VDVVEY 265

RESULT 26  
US-09-897-516A-6610  
;; Sequence 6610, Application US/09897516A  
;; GENERAL INFORMATION:  
;; APPLICANT: Corbin, David R.  
;; APPLICANT: Goldman, Barry S.  
;; APPLICANT: Hinkle, Gregory J.  
;; APPLICANT: Huesling, Joseph E.  
;; APPLICANT: Malvar, Thomas M.  
;; APPLICANT: Krasomil-Osterfeld, Karina C.  
;; APPLICANT: Slater, Steven C.  
;; APPLICANT: Spiridonov, Sergei  
;; TITLE OF INVENTION: Xenorhabdus sp. Genome Sequences And Uses Thereof  
;; FILE REFERENCE: 38-21(51847)B  
;; CURRENT APPLICATION NUMBER: US/09/897,516A  
;; CURRENT FILING DATE: 2001-06-29  
;; PRIOR APPLICATION NUMBER: US 60/215,161  
;; PRIOR FILING DATE: 2000-05-30  
;; NUMBER OF SEQ ID NOS: 8415  
;; SEQ ID NO 6610  
;; LENGTH: 316  
;; TYPE: PRT  
;; ORGANISM: Xenorhabdus sp.  
US-09-897-516A-6610

Query Match 86.7%; Score 26; DB 5; Length 316;  
Best Local Similarity 66.7%; Pred. No. 2.3e+03;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVDVEY 6  
|||:|  
Db 185 SVDIDY 190

RESULT 27  
US-10-425-114A-40092  
; Sequence 40092, Application US/10425114A  
; GENERAL INFORMATION:  
; APPLICANT: Liu, Jingdong  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Screen, Steven E  
; APPLICANT: Tabaska, Jack E  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(53313)B  
; CURRENT APPLICATION NUMBER: US/10/425.114A  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 73128  
; SEQ ID NO 40092  
; LENGTH: 337  
; TYPE: PRT  
; ORGANISM: Glycine max  
; FEATURE:  
; OTHER INFORMATION: Clone ID: 700995187\_FLI.pap  
US-10-425-114A-40092

Query Match 86.7%; Score 26; DB 6; Length 337;  
Best Local Similarity 66.7%; Pred. No. 2.4e+03;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVDVEY 6  
|||:|  
Db 59 SVDIQY 64

RESULT 28  
US-10-425-114A-64094  
; Sequence 64094, Application US/10425114A  
; GENERAL INFORMATION:  
; APPLICANT: Liu, Jingdong  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Screen, Steven E  
; APPLICANT: Tabaska, Jack E  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(53313)B  
; CURRENT APPLICATION NUMBER: US/10/425.114A  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 73128  
; SEQ ID NO 64094  
; LENGTH: 341  
; TYPE: PRT  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: LTB3354-084-A4\_FLI.pap  
US-10-425-114A-64094

Query Match 86.7%; Score 26; DB 6; Length 341;  
Best Local Similarity 100.0%; Pred. No. 2.4e+03;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VDVVEY 6  
|||:|  
Db 208 VDVVEY 212

RESULT 29  
US-10-739-930-10318  
; Sequence 10318, Application US/10739930  
; GENERAL INFORMATION:  
; APPLICANT: Kovalic, David K.  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH  
; FILE REFERENCE: 38-21(53377)B  
; CURRENT APPLICATION NUMBER: US/10/739,930  
; CURRENT FILING DATE: 2003-12-18  
; NUMBER OF SEQ ID NOS: 11088  
; SEQ ID NO 10318  
; LENGTH: 366  
; TYPE: PRT  
; ORGANISM: Triticum aestivum  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (1)..(366)  
; OTHER INFORMATION: unsure at all Xaa locations  
; FEATURE:  
; OTHER INFORMATION: Clone ID: TRIAE-23APR03-C3611\_1.p  
US-10-739-930-10318

Query Match 86.7%; Score 26; DB 6; Length 366;  
Best Local Similarity 100.0%; Pred. No. 2.5e+03;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VDVVEY 6  
|||:|  
Db 198 VDVVEY 202

RESULT 30  
US-10-415-182A-9892  
; Sequence 9892, Application US/10415182A  
; GENERAL INFORMATION:  
; APPLICANT: Telford, John  
; TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B  
; FILE REFERENCE:  
; CURRENT APPLICATION NUMBER: US/10/415,182A  
; CURRENT FILING DATE: 2003-12-09  
; PRIOR APPLICATION NUMBER: GB-0026333.5  
; PRIOR FILING DATE: 2000-10-27  
; PRIOR APPLICATION NUMBER: GB-0028727.6  
; PRIOR FILING DATE: 2000-11-24  
; PRIOR APPLICATION NUMBER: GB-0105640.7  
; PRIOR FILING DATE: 2001-03-07  
; NUMBER OF SEQ ID NOS: 12024  
; SOFTWARE: SeqWin99, version 1.02  
; SEQ ID NO 9892  
; LENGTH: 408  
; TYPE: PRT  
; ORGANISM: Streptococcus agalactiae  
US-10-415-182A-9892

Query Match 86.7%; Score 26; DB 6; Length 408;  
Best Local Similarity 66.7%; Pred. No. 2.6e+03;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVDVEY 6  
|||:|  
Db 193 AVDIEY 198

RESULT 31  
US-10-415-182A-2698  
; Sequence 2698, Application US/10415182A  
; GENERAL INFORMATION:  
; APPLICANT: Telford, John  
; TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM STREPTOCOCCUS GROUPS A & B  
; FILE REFERENCE:

; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Incyte ID No: LI:200704.1.orf3:2001MAY17  
US-10-473-040-683  
Query Match 86.7%; Score 26; DB 6; Length 428;  
Best Local Similarity 66.7%; Pred. No. 2.6e+03;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SVDVEY 6  
Db 398 SIDLEY 403  
RESULT 33  
US-60-479-962-447  
; Sequence 447, Application US/60479962  
; GENERAL INFORMATION:  
; APPLICANT: Monsanto Technology, LLC  
; APPLICANT: Laurie, Cathy C  
; APPLICANT: LeDeaux, John R  
; APPLICANT: Fabbri, Brandon J  
; TITLE OF INVENTION: Nucleic Acid Molecules Associated with Protein in Plants  
; FILE REFERENCE: 38-21(53372)A  
; CURRENT APPLICATION NUMBER: US/60/479,962  
; CURRENT FILING DATE: 2003-06-19  
; NUMBER OF SEQ ID NOS: 488  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 447  
; LENGTH: 442  
; TYPE: PRT  
; ORGANISM: Zea mays  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (81)..(81)  
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (304)..(304)  
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid  
US-60-479-962-447  
Query Match 86.7%; Score 26; DB 7; Length 442;  
Best Local Similarity 100.0%; Pred. No. 2.6e+03;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 VDVVEY 6  
Db 386 VDVVEY 390  
RESULT 34  
US-10-739-930-5786  
; Sequence 5786, Application US/10739930  
; GENERAL INFORMATION:  
; APPLICANT: Kovalic, David K.  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH  
; FILE REFERENCE: 38-21(53377)B  
; CURRENT APPLICATION NUMBER: US/10/739,930  
; CURRENT FILING DATE: 2003-12-18  
; NUMBER OF SEQ ID NOS: 11088  
; SEQ ID NO 5786  
; LENGTH: 455  
; TYPE: PRT  
; ORGANISM: Arabidopsis thaliana  
; FEATURE:  
; OTHER INFORMATION: Clone ID: ARATH-23APR03-C14066\_1.p  
US-10-739-930-5786  
Query Match 86.7%; Score 26; DB 6; Length 455;  
Best Local Similarity 100.0%; Pred. No. 2.6e+03;

; CURRENT APPLICATION NUMBER: US/10/415,182A  
; CURRENT FILING DATE: 2003-12-09  
; PRIOR APPLICATION NUMBER: GB-0026333.5  
; PRIOR FILING DATE: 2000-10-27  
; PRIOR APPLICATION NUMBER: GB-0028727.6  
; PRIOR FILING DATE: 2000-11-24  
; PRIOR APPLICATION NUMBER: GB-0105640.7  
; PRIOR FILING DATE: 2001-03-07  
; NUMBER OF SEQ ID NOS: 12024  
; SOFTWARE: SeqWin99, version 1.02  
; SEQ ID NO 2698  
; LENGTH: 420  
; TYPE: PRT  
; ORGANISM: Streptococcus agalactiae  
US-10-415-182A-2698  
Query Match 86.7%; Score 26; DB 6; Length 420;  
Best Local Similarity 66.7%; Pred. No. 2.6e+03;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SVDVEY 6  
Db 205 AVDIEY 210  
RESULT 32  
US-10-473-040-683  
; Sequence 683, Application US/10473040  
; GENERAL INFORMATION:  
; APPLICANT: INCYTE CORPORATION; DAFFO, Abel;  
; APPLICANT: JONES, Anissa L.; TRAN, Alanna-Phung B.;  
; APPLICANT: DAHL, Christopher R.; GIETZEN, Darryl R.;  
; APPLICANT: CHINN, Joyce; DUFOUR, Gerard E.;  
; APPLICANT: JACKSON, Jennifer L.; YU, Jimmy Y.;  
; APPLICANT: TUASON, Olivia; YAP, Pierre E.;  
; APPLICANT: AMSHEY, Stefan R.; DAUGHERTY, Sean C.;  
; APPLICANT: DAM, Tam C.; LIU, Tommy F.;  
; APPLICANT: NGUYEN, Duy-Viet A.; KLEBEELD, Yael;  
; APPLICANT: GERSTIN, JR., Edward H.; PERALTA, Careyana H.;  
; APPLICANT: DAVID, Marie H.; LEWIS, Samantha A.;  
; APPLICANT: CHEN, Alice J.; PANZER, Scott R.;  
; APPLICANT: HARRIS, Bernard; MULLAHY-FLORES, Vincent Z.;  
; APPLICANT: MARWAHA, Rakesh; LO, Audrey;  
; APPLICANT: LAN, Ruth Y.; URASHKA, Michael E.  
; TITLE OF INVENTION: MOLECULES FOR DISEASE DETECTION AND TREATMENT  
; FILE REFERENCE: PT-1231 USN  
; CURRENT APPLICATION NUMBER: US/10/473,040  
; CURRENT FILING DATE: 2003-09-26  
; PRIOR APPLICATION NUMBER: PCT/US02/09944  
; PRIOR FILING DATE: 2002-03-27  
; PRIOR APPLICATION NUMBER: 60/279,619  
; PRIOR FILING DATE: 2001-03-28  
; PRIOR APPLICATION NUMBER: 60/280,067  
; PRIOR FILING DATE: 2001-03-29  
; PRIOR APPLICATION NUMBER: 60/280,068  
; PRIOR FILING DATE: 2001-03-29  
; PRIOR APPLICATION NUMBER: 60/291,280  
; PRIOR FILING DATE: 2001-05-16  
; PRIOR APPLICATION NUMBER: 60/291,849  
; PRIOR FILING DATE: 2001-05-17  
; PRIOR APPLICATION NUMBER: 60/291,829  
; PRIOR FILING DATE: 2001-05-17  
; PRIOR APPLICATION NUMBER: 60/299,428  
; PRIOR FILING DATE: 2001-06-19  
; PRIOR APPLICATION NUMBER: 60/300,001  
; PRIOR FILING DATE: 2001-06-20  
; PRIOR APPLICATION NUMBER: 60/299,776  
; PRIOR FILING DATE: 2001-06-20  
; NUMBER OF SEQ ID NOS: 792  
; SOFTWARE: PERL Program  
; SEQ ID NO 683  
; LENGTH: 428  
; TYPE: PRT

```
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 VDVEY 6
Db 345 VDVEY 349

RESULT 35
US-10-679-063-16687
; Sequence 16687, Application US/10679063
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52054)B
; CURRENT APPLICATION NUMBER: US/10/679,063
; CURRENT FILING DATE: 2003-10-02
; PRIOR APPLICATION NUMBER: 60/415,758
; PRIOR FILING DATE: 2002-10-02
; NUMBER OF SEQ ID NOS: 27373
; SEQ ID NO 16687
; LENGTH: 460
; TYPE: PRT
; ORGANISM: Magnetospirillum magnetotacticum
US-10-679-063-16687

Query Match 86.7%; Score 26; DB 6; Length 460;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 VDVEY 6
Db 42 VDVEY 46

RESULT 36
US-10-679-063-2191
; Sequence 2191, Application US/10679063
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52054)B
; CURRENT APPLICATION NUMBER: US/10/679,063
; CURRENT FILING DATE: 2003-10-02
; PRIOR APPLICATION NUMBER: 60/415,758
; PRIOR FILING DATE: 2002-10-02
; NUMBER OF SEQ ID NOS: 27373
; SEQ ID NO 2191
; LENGTH: 532
; TYPE: PRT
; ORGANISM: Glycine max
; NAME/KEY: unsure
; LOCATION: (1)...(532)
; OTHER INFORMATION: unsure at all Xaa locations
US-10-679-063-2191

Query Match 86.7%; Score 26; DB 6; Length 532;
Best Local Similarity 66.7%; Pred. No. 2.8e+03;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Qy 1 SVDVEY 6
Db 254 SVDIQY 259

RESULT 37
US-10-472-928-3056
; Sequence 3056, Application US/10472928
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; TITLE OF INVENTION: THE INSTITUTE FOR GENOMIC RESEARCH
; APPLICANT: STREPTOCOCCUS PNEUMONIAE PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE: P026326W0
```

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; CURRENT APPLICATION NUMBER: US/10/472,928
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: GB-0107658.7
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 4979
; SOFTWARE: SeqMin99, version 1.03
; SEQ ID NO 3056
; LENGTH: 572
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
; FEATURE:
; OTHER INFORMATION: phosphoglucomutase (pgm)
; OTHER INFORMATION: Cellular location: cytoplasm
; OTHER INFORMATION: Similar to strain R6 sequence 15903394 (O.E+01)
US-10-472-928-3056

Query Match 86.7%; Score 26; DB 6; Length 572;
Best Local Similarity 66.7%; Pred. No. 2.9e+03;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Qy 1 SVDVEY 6
Db 204 AVDIEY 209

RESULT 38
US-10-679-063-2707
; Sequence 2707, Application US/10679063
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52054)B
; CURRENT APPLICATION NUMBER: US/10/679,063
; CURRENT FILING DATE: 2003-10-02
; PRIOR APPLICATION NUMBER: 60/415,758
; PRIOR FILING DATE: 2002-10-02
; NUMBER OF SEQ ID NOS: 27373
; SEQ ID NO 2707
; LENGTH: 597
; TYPE: PRT
; ORGANISM: Glycine max
US-10-679-063-2707

Query Match 86.7%; Score 26; DB 6; Length 597;
Best Local Similarity 66.7%; Pred. No. 2.9e+03;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Qy 1 SVDVEY 6
Db 319 SVDIQY 324

RESULT 39
US-10-451-168-56
; Sequence 56, Application US/10451168
; GENERAL INFORMATION:
; APPLICANT: SMITHKLINE BEECHAM CORPORATION
; APPLICANT: SMITHKLINE BEECHAM p.l.c.
; APPLICANT: GLAXO GROUP LIMITED
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GPS0039
; CURRENT APPLICATION NUMBER: US/10/451,168
; CURRENT FILING DATE: 2003-11-12
; PRIOR APPLICATION NUMBER: PCT/US01/49232
; PRIOR FILING DATE: 2000-12-17
; PRIOR APPLICATION NUMBER: 60/256,710
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/257,048
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: 60/260,482
; PRIOR FILING DATE: 2001-01-09
; PRIOR APPLICATION NUMBER: 60/264,922
; PRIOR FILING DATE: 2001-01-30
```

; PRIOR APPLICATION NUMBER: 60/266,797  
; PRIOR FILING DATE: 2001-02-06  
; PRIOR APPLICATION NUMBER: 60/276,988  
; PRIOR FILING DATE: 2001-03-19  
; PRIOR APPLICATION NUMBER: 60/281,535  
; PRIOR FILING DATE: 2001-04-04  
; PRIOR APPLICATION NUMBER: 60/289,622  
; PRIOR FILING DATE: 2002-06-28  
; NUMBER OF SEQ ID NOS: 110  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 56  
; LENGTH: 606  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-451-168-56

Query Match 86.7%; Score 26; DB 6; Length 606;  
Best Local Similarity 66.7%; Pred. No. 2.9e+03;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVEY 6  
|:|:|  
Db 576 SIDLEY 581

RESULT 40  
US-10-451-168-57  
; Sequence 57, Application US/10451168  
; GENERAL INFORMATION:  
; APPLICANT: SMITHKLINE BEECHAM CORPORATION  
; APPLICANT: SMITHKLINE BEECHAM p.l.c.  
; APPLICANT: GLAXO GROUP LIMITED  
; TITLE OF INVENTION: NOVEL COMPOUNDS  
; FILE REFERENCE: GF50039  
; CURRENT APPLICATION NUMBER: US/10/451,168  
; CURRENT FILING DATE: 2003-11-12  
; PRIOR APPLICATION NUMBER: PCT/US01/49232  
; PRIOR FILING DATE: 2000-12-17  
; PRIOR APPLICATION NUMBER: 60/256,710  
; PRIOR FILING DATE: 2000-12-19  
; PRIOR APPLICATION NUMBER: 60/257,048  
; PRIOR FILING DATE: 2000-12-20  
; PRIOR APPLICATION NUMBER: 60/260,482  
; PRIOR FILING DATE: 2001-01-09  
; PRIOR APPLICATION NUMBER: 60/264,922  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: 60/266,797  
; PRIOR FILING DATE: 2001-02-06  
; PRIOR APPLICATION NUMBER: 60/276,988  
; PRIOR FILING DATE: 2001-03-19  
; PRIOR APPLICATION NUMBER: 60/281,535  
; PRIOR FILING DATE: 2001-04-04  
; PRIOR APPLICATION NUMBER: 60/289,622  
; PRIOR FILING DATE: 2002-06-28  
; NUMBER OF SEQ ID NOS: 110  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 57  
; LENGTH: 606  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-451-168-57

Query Match 86.7%; Score 26; DB 6; Length 606;  
Best Local Similarity 66.7%; Pred. No. 2.9e+03;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVEY 6  
|:|:|  
Db 576 SIDLEY 581

RESULT 41  
US-09-614-150A-18810

; Sequence 18810, Application US/09614150A  
; GENERAL INFORMATION:  
; APPLICANT: Venter, J. Craig  
; APPLICANT: et al.  
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID  
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE  
; FILE REFERENCE: CL000728  
; CURRENT APPLICATION NUMBER: US/09/614,150A  
; CURRENT FILING DATE: 2000-07-11  
; PRIOR APPLICATION NUMBER: 60/157,832  
; PRIOR FILING DATE: 1999-10-05  
; PRIOR APPLICATION NUMBER: 60/160,191  
; PRIOR FILING DATE: 1999-10-19  
; PRIOR APPLICATION NUMBER: 60/161,932  
; PRIOR FILING DATE: 1999-10-28  
; PRIOR APPLICATION NUMBER: 60/164,769  
; PRIOR FILING DATE: 1999-11-12  
; PRIOR APPLICATION NUMBER: 60/173,383  
; PRIOR FILING DATE: 1999-12-28  
; PRIOR APPLICATION NUMBER: 60/175,693  
; PRIOR FILING DATE: 2000-01-12  
; PRIOR APPLICATION NUMBER: 60/184,831  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: 60/191,637  
; PRIOR FILING DATE: 2000-03-23  
; NUMBER OF SEQ ID NOS: 43008  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 18810  
; LENGTH: 615  
; TYPE: PRT  
; ORGANISM: DROSOPHILA  
US-09-614-150A-18810

Query Match 86.7%; Score 26; DB 5; Length 615;  
Best Local Similarity 83.3%; Pred. No. 2.9e+03;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SVDVEY 6  
|:|:|  
Db 499 SADVEY 504

RESULT 42  
US-09-614-150A-3981  
; Sequence 3981, Application US/09614150A  
; GENERAL INFORMATION:  
; APPLICANT: Venter, J. Craig  
; APPLICANT: et al.  
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID  
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE  
; FILE REFERENCE: CL000728  
; CURRENT APPLICATION NUMBER: US/09/614,150A  
; CURRENT FILING DATE: 2000-07-11  
; PRIOR APPLICATION NUMBER: 60/157,832  
; PRIOR FILING DATE: 1999-10-05  
; PRIOR APPLICATION NUMBER: 60/160,191  
; PRIOR FILING DATE: 1999-10-19  
; PRIOR APPLICATION NUMBER: 60/161,932  
; PRIOR FILING DATE: 1999-10-28  
; PRIOR APPLICATION NUMBER: 60/164,769  
; PRIOR FILING DATE: 1999-11-12  
; PRIOR APPLICATION NUMBER: 60/173,383  
; PRIOR FILING DATE: 1999-12-28  
; PRIOR APPLICATION NUMBER: 60/175,693  
; PRIOR FILING DATE: 2000-01-12  
; PRIOR APPLICATION NUMBER: 60/184,831  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: 60/191,637  
; PRIOR FILING DATE: 2000-03-23  
; NUMBER OF SEQ ID NOS: 43008  
; SOFTWARE: FastSeq for Windows Version 4.0

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; SEQ ID NO 3981
; LENGTH: 633
; TYPE: PRT
; ORGANISM: DROSOPHILA
US-09-614-150A-3981

Query Match      86.7%; Score 26; DB 5; Length 633;
Best Local Similarity 66.7%; Pred. No. 3e+03;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVDVEY 6
Db 449 SIDVDY 454

RESULT 43
US-60-495-589-168
; Sequence 168, Application US/60495589
; GENERAL INFORMATION:
; APPLICANT: Progulske-Fox, Ann
; APPLICANT: Hillman, Jeffrey D.
; APPLICANT: Handfield, Martin
; TITLE OF INVENTION: IDENTIFICATION OF PORPHYROMONAS GINGIVALIS VIRULENCE POLYNUCLEOTIDE
; TITLE OF INVENTION: DIAGNOSIS, TREATMENT, AND MONITORING OF PERIODONTAL DISEASES
; FILE REFERENCE: 02-042
; CURRENT APPLICATION NUMBER: US/60/495,589
; CURRENT FILING DATE: 2003-08-15
; NUMBER OF SEQ ID NOS: 354
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 168
; LENGTH: 673
; TYPE: PRT
; ORGANISM: Porphyromonas gingivalis
US-60-495-589-168

Query Match      86.7%; Score 26; DB 7; Length 673;
Best Local Similarity 83.3%; Pred. No. 3e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVDVEY 6
Db 385 SVDVEF 390

RESULT 44
US-10-418-861B-42
; Sequence 42, Application US/10418861B
; GENERAL INFORMATION:
; APPLICANT: da Silva, Ana Claudia Raseira
; APPLICANT: Farah, Shaker Chuck
; APPLICANT: Quaggio, Ronaldo Bento
; APPLICANT: Reinach, Fernando de Castro
; APPLICANT: Ferro, Jesus Aparecido
; APPLICANT: De Oliveira, Julio Cezar Franco
; APPLICANT: Setubal Joao Luiz
; APPLICANT: Furlan, Luiz Roberto
; TITLE OF INVENTION: Isolated Xanthomonas nucleic acid molecules, proteins encoded the
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: FAPESP 205.1 US
; CURRENT APPLICATION NUMBER: US/10/418,861B
; CURRENT FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: US 60/374,620
; PRIOR FILING DATE: 2002-04-22
; NUMBER OF SEQ ID NOS: 85
; SEQ ID NO 42
; LENGTH: 676
; TYPE: PRT
; ORGANISM: Xanthomonas
; FEATURE:
US-10-418-861B-42

Query Match      86.7%; Score 26; DB 6; Length 676;

Best Local Similarity 100.0%; Pred. No. 3e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VDVEY 6
Db 217 VDVEY 221

RESULT 45
US-10-475-292-167
; Sequence 167, Application US/10475292
; GENERAL INFORMATION:
; APPLICANT: AI Xiclan et al.
; TITLE OF INVENTION: PRIMARY NUCLEOTIDE SEQUENCE OF THE
; TITLE OF INVENTION: AGROTIS SEGETUM GRANULOSIS VIRUS (AsGV), INSECTICIDE
; TITLE OF INVENTION: DISCOVERY SYSTEMS CONTAINING THIS SEQUENCE AND PREVENTION
; TITLE OF INVENTION: AND CONTROLLING KITS FOR AGROTIS SEGETUM INSECT OUTBREAK AND
; TITLE OF INVENTION: SPREAD
; FILE REFERENCE: CL001308-US
; CURRENT APPLICATION NUMBER: US/10/475,292
; CURRENT FILING DATE: 2003-10-20
; PRIOR APPLICATION NUMBER: PCT/US01/32153
; PRIOR FILING DATE: 2001-10-17
; PRIOR APPLICATION NUMBER: CN01112663.9
; PRIOR FILING DATE: 2001-04-18
; NUMBER OF SEQ ID NOS: 217
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 167
; LENGTH: 883
; TYPE: PRT
; ORGANISM: AsGV
US-10-475-292-167

Query Match      86.7%; Score 26; DB 6; Length 883;
Best Local Similarity 66.7%; Pred. No. 3.3e+03;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVDVEY 6
Db 204 SVDIDY 209

RESULT 46
US-09-581-286A-442
; Sequence 442, Application US/09581286A
; GENERAL INFORMATION:
; APPLICANT: ROSS, BRUCE C.
; APPLICANT: BARR, IAN G.
; APPLICANT: PATTERSON, MICHELLE A.
; APPLICANT: AGIUS, CATHERINE T.
; APPLICANT: ROTHEN, LINDA J.
; APPLICANT: MARGETTS, MAL B.
; APPLICANT: HOCKING, DIANNA M.
; APPLICANT: WEBB, ELIZABETH A.
; TITLE OF INVENTION: PORPHYROMONAS GINGIVALIS POLYPEPTIDES AND NUCLEOTIDES
; FILE REFERENCE: 4137-3
; CURRENT APPLICATION NUMBER: US/09/581,286A
; CURRENT FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: PCT/AU98/01023
; PRIOR FILING DATE: 1998-12-10
; PRIOR APPLICATION NUMBER: AU PP 0839
; PRIOR FILING DATE: 1997-12-10
; PRIOR APPLICATION NUMBER: AU PP 1182
; PRIOR FILING DATE: 1997-12-31
; PRIOR APPLICATION NUMBER: AU PP 1846
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: AU PP 2264
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: AU PP 2911
; PRIOR FILING DATE: 1998-04-09
; PRIOR APPLICATION NUMBER: AU PP 3128
; PRIOR FILING DATE: 1998-04-23
; PRIOR APPLICATION NUMBER: AU PP 3338
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/ PRIOR FILING DATE: 1998-05-05
/ PRIOR APPLICATION NUMBER: AU PP 3654
/ PRIOR FILING DATE: 1998-05-22
/ PRIOR APPLICATION NUMBER: AU PP 4917
/ PRIOR FILING DATE: 1998-07-29
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 721
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 442
/ LENGTH: 891
/ TYPE: PRT
/ ORGANISM: Porphyromonas gingivalis
US-09-581-286A-442

Query Match      86.7%; Score 26; DB 5; Length 891;
Best Local Similarity 66.7%; Pred. No. 3.3e+03;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVEY 6
Db 451 TVDIY 456

RESULT 47
US-09-581-286A-316
/ Sequence 316, Application US/09581286A
/ GENERAL INFORMATION:
/ APPLICANT: ROSS, BRUCE C.
/ APPLICANT: BARR, IAN G.
/ APPLICANT: PATTERSON, MICHELLE A.
/ APPLICANT: AGIUS, CATHERINE T.
/ APPLICANT: ROTHGEL, LINDA J.
/ APPLICANT: MARGETTS, MAL B.
/ APPLICANT: HOCKING, DIANNA M.
/ APPLICANT: WEBB, ELIZABETH A.
/ TITLE OF INVENTION: PORPHYROMONAS GINGIVALIS POLYPEPTIDES AND NUCLEOTIDES
/ FILE REFERENCE: 4137-3
/ CURRENT APPLICATION NUMBER: US/09/581.286A
/ CURRENT FILING DATE: 2000-06-28
/ PRIOR APPLICATION NUMBER: PCT/AU98/01023
/ PRIOR FILING DATE: 1998-12-10
/ PRIOR APPLICATION NUMBER: AU PP 0839
/ PRIOR FILING DATE: 1997-12-10
/ PRIOR APPLICATION NUMBER: AU PP 1182
/ PRIOR FILING DATE: 1997-12-31
/ PRIOR APPLICATION NUMBER: AU PP 1846
/ PRIOR FILING DATE: 1998-01-30
/ PRIOR APPLICATION NUMBER: AU PP 2264
/ PRIOR FILING DATE: 1998-03-10
/ PRIOR APPLICATION NUMBER: AU PP 2911
/ PRIOR FILING DATE: 1998-04-09
/ PRIOR APPLICATION NUMBER: AU PP 3128
/ PRIOR FILING DATE: 1998-04-23
/ PRIOR APPLICATION NUMBER: AU PP 3338
/ PRIOR FILING DATE: 1998-05-05
/ PRIOR APPLICATION NUMBER: AU PP 3654
/ PRIOR FILING DATE: 1998-05-22
/ PRIOR APPLICATION NUMBER: AU PP 4917
/ PRIOR FILING DATE: 1998-07-29
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 721
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 316
/ LENGTH: 899
/ TYPE: PRT
/ ORGANISM: Porphyromonas gingivalis
US-09-581-286A-316

Query Match      86.7%; Score 26; DB 5; Length 899;
Best Local Similarity 66.7%; Pred. No. 3.3e+03;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVEY 6
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Db 459 TVDIY 464

RESULT 48
US-09-614-150A-16857
/ Sequence 16857, Application US/09614150A
/ GENERAL INFORMATION:
/ APPLICANT: Venter, J. Craig
/ APPLICANT: et al.
/ TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
/ TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
/ TITLE OF INVENTION: DROSOPHILA GENES.
/ FILE REFERENCE: CL000728
/ CURRENT APPLICATION NUMBER: US/09/614,150A
/ CURRENT FILING DATE: 2000-07-11
/ PRIOR APPLICATION NUMBER: 60/157,832
/ PRIOR FILING DATE: 1999-10-05
/ PRIOR APPLICATION NUMBER: 60/160,191
/ PRIOR FILING DATE: 1999-10-19
/ PRIOR APPLICATION NUMBER: 60/161,932
/ PRIOR FILING DATE: 1999-10-28
/ PRIOR APPLICATION NUMBER: 60/164,769
/ PRIOR FILING DATE: 1999-11-12
/ PRIOR APPLICATION NUMBER: 60/173,383
/ PRIOR FILING DATE: 1999-12-28
/ PRIOR APPLICATION NUMBER: 60/175,693
/ PRIOR FILING DATE: 2000-01-12
/ PRIOR APPLICATION NUMBER: 60/184,831
/ PRIOR FILING DATE: 2000-02-24
/ PRIOR APPLICATION NUMBER: 60/191,637
/ PRIOR FILING DATE: 2000-03-23
/ NUMBER OF SEQ ID NOS: 43008
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 16857
/ LENGTH: 1082
/ TYPE: PRT
/ ORGANISM: DROSOPHILA
US-09-614-150A-16857

Query Match      86.7%; Score 26; DB 5; Length 1082;
Best Local Similarity 83.3%; Pred. No. 3.6e+03;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SVDVEY 6
Db 858 SVDTEY 863

RESULT 49
US-09-614-150A-18237
/ Sequence 18237, Application US/09614150A
/ GENERAL INFORMATION:
/ APPLICANT: Venter, J. Craig
/ APPLICANT: et al.
/ TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
/ TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
/ TITLE OF INVENTION: DROSOPHILA GENES.
/ FILE REFERENCE: CL000728
/ CURRENT APPLICATION NUMBER: US/09/614,150A
/ CURRENT FILING DATE: 2000-07-11
/ PRIOR APPLICATION NUMBER: 60/157,832
/ PRIOR FILING DATE: 1999-10-05
/ PRIOR APPLICATION NUMBER: 60/160,191
/ PRIOR FILING DATE: 1999-10-19
/ PRIOR APPLICATION NUMBER: 60/161,932
/ PRIOR FILING DATE: 1999-10-28
/ PRIOR APPLICATION NUMBER: 60/164,769
/ PRIOR FILING DATE: 1999-11-12
/ PRIOR APPLICATION NUMBER: 60/173,383
/ PRIOR FILING DATE: 1999-12-28
/ PRIOR APPLICATION NUMBER: 60/175,693
/ PRIOR FILING DATE: 2000-01-12
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; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18237
; LENGTH: 1137
; TYPE: PRT
; ORGANISM: DROSOPHILA
US-09-614-150A-18237

Query Match      86.7%; Score 26; DB 5; Length 1137;
Best Local Similarity 66.7%; Pred. No. 3.6e+03;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVEY 6
Db 122 TVDIEY 127

RESULT 50
US-10-472-928-972
; Sequence 972, Application US/10472928
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: THE INSTITUTE FOR GENOMIC RESEARCH
; TITLE OF INVENTION: STREPTOCOCCUS PNEUMONIAE PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE: P026926WO
; CURRENT APPLICATION NUMBER: US/10/472,928
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: GB-0107658.7
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 4979
; SOFTWARE: SeqWin99, version 1.03
; SEQ ID NO 972
; LENGTH: 50
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
; FEATURE:
; OTHER INFORMATION: hypothetical protein
; OTHER INFORMATION: Cellular location: cytoplasm
; OTHER INFORMATION: Similar to strain R6 sequence 15902521 (6.E-86)
US-10-472-928-972

Query Match      83.3%; Score 25; DB 6; Length 50;
Best Local Similarity 80.0%; Pred. No. 1.7e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDVVEY 6
Db 26 VDIEY 30
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Search completed: January 20, 2004, 14:01:56  
Job time : 25 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 20, 2004, 13:55:27 ; Search time 173 Seconds

(without alignments)

31.558 Million cell updates/sec

Title: US-09-919-703-1

Perfect score: 30

Sequence: 1 SVDVEY 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 5728757 seqs, 909918778 residues

Total number of hits satisfying chosen parameters: 5728757

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 75 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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2	30	100.0	6	24	US-09-919-703-1	Sequence 1, Appli
3	30	100.0	16	24	US-09-919-703-5	Sequence 5, Appli
4	30	100.0	18	9	US-08-567-943-5	Sequence 5, Appli
5	30	100.0	20	9	US-08-567-943-6	Sequence 6, Appli
6	30	100.0	20	24	US-09-919-703-6	Sequence 6, Appli
7	30	100.0	21	9	US-08-567-943-7	Sequence 7, Appli
8	30	100.0	21	24	US-09-919-703-7	Sequence 7, Appli
9	30	100.0	128	22	US-09-791-537-83460	Sequence 83460, A
10	30	100.0	137	22	US-09-791-537-12562	Sequence 12562, A
11	30	100.0	138	22	US-09-791-537-104248	Sequence 104248, A
12	30	100.0	362	22	US-09-791-537-23287	Sequence 23287, A
13	30	100.0	372	20	US-09-658-681-3	Sequence 3, Appli
14	30	100.0	384	20	US-09-658-681-4	Sequence 4, Appli
15	30	100.0	401	20	US-09-658-681-1	Sequence 1, Appli
16	30	100.0	413	9	US-08-567-943-12	Sequence 12, Appli
17	30	100.0	413	20	US-09-658-681-2	Sequence 2, Appli
18	30	100.0	413	24	US-09-919-703-12	Sequence 12, Appli
19	30	100.0	413	29	US-10-360-101-264	Sequence 264, Appl
20	30	100.0	414	1	PCT-US93-09502-1	Sequence 1, Appli
21	30	100.0	414	5	US-07-956-692A-9	Sequence 9, Appli
22	30	100.0	414	5	US-08-128-299-1	Sequence 1, Appli
23	30	100.0	414	18	US-09-438-136-252	Sequence 252, App
24	30	100.0	414	18	US-09-438-136-253	Sequence 253, App
25	30	100.0	414	18	US-09-471-349-2	Sequence 2, Appli
26	30	100.0	414	20	US-09-633-516B-7	Sequence 7, Appli
27	30	100.0	414	20	US-09-633-516B-8	Sequence 8, Appli
28	30	100.0	414	22	US-09-791-537-418	Sequence 418, App
29	30	100.0	414	24	US-09-940-235-2	Sequence 2, Appli
30	30	100.0	414	29	US-10-300-215-252	Sequence 252, App
31	30	100.0	414	29	US-10-300-215-253	Sequence 253, App
32	30	100.0	414	31	US-10-631-558-2	Sequence 2, Appli
33	30	100.0	415	17	US-09-305-958-4	Sequence 4, Appli
34	30	100.0	415	17	US-09-305-970-5	Sequence 5, Appli
35	30	100.0	415	22	US-09-791-537-45189	Sequence 45189, A
36	30	100.0	440	22	US-09-791-537-45189	Sequence 45189, A
37	30	100.0	440	22	US-09-791-537-45189	Sequence 45189, A
38	30	100.0	440	22	US-09-791-537-45192	Sequence 45192, A
39	30	100.0	891	20	US-09-609-360B-25	Sequence 25, Appl
40	30	100.0	891	20	US-09-609-360C-25	Sequence 25, Appl
41	30	100.0	891	20	US-09-609-360D-25	Sequence 25, Appl
42	30	100.0	891	22	US-09-791-537-145994	Sequence 145994, A
43	30	100.0	891	23	US-09-862-027-25	Sequence 25, Appl
44	30	100.0	1274	22	US-09-791-537-105510	Sequence 105510, A
45	29	96.7	43	32	US-60-139-670-115	Sequence 115, App
46	29	96.7	43	32	US-60-143-753-234	Sequence 234, App
47	29	96.7	66	32	US-60-143-989-236	Sequence 236, App
48	29	96.7	68	32	US-60-145-138-515	Sequence 515, App
49	29	96.7	68	32	US-60-145-989-317	Sequence 317, App
50	29	96.7	72	30	US-10-424-599-271681	Sequence 271681, A
51	29	96.7	80	16	US-09-252-691-10860	Sequence 10860, A
52	29	96.7	80	16	US-09-252-691C-10860	Sequence 10860, A
53	29	96.7	80	30	US-10-417-886-10860	Sequence 10860, A
54	29	96.7	374	30	US-10-424-599-218318	Sequence 218318, A
55	29	96.7	520	20	US-09-614-150-25695	Sequence 25695, A
56	29	96.7	520	32	US-60-191-637-25822	Sequence 25822, A
57	29	96.7	520	32	US-60-191-661-20431	Sequence 20431, A
58	29	96.7	796	24	US-09-935-625-23345	Sequence 23345, A
59	29	96.7	835	24	US-09-935-625-23344	Sequence 23344, A
60	29	96.7	836	24	US-09-935-625-23343	Sequence 23343, A
61	29	96.7	1190	20	US-09-614-150-3243	Sequence 3243, Ap
62	29	96.7	1190	22	US-09-791-537-12970	Sequence 12970, A
63	29	96.7	1190	32	US-60-173-464-2708	Sequence 2708, Ap
64	29	96.7	1190	32	US-60-191-637-3252	Sequence 3252, Ap
65	29	96.7	1190	32	US-60-191-681-2610	Sequence 2610, Ap
66	29	96.7	1207	29	US-10-369-493-5723	Sequence 5723, Ap
67	29	96.7	1207	32	US-60-360-039-5723	Sequence 5723, Ap
68	29	96.7	1595	22	US-09-791-537-61747	Sequence 61747, A
69	28	93.3	280	1	PCT-US00-35180-14	Sequence 14, Appl
70	28	93.3	280	20	US-09-689-952-14	Sequence 14, Appl
71	28	93.3	397	28	US-10-282-122A-53090	Sequence 53090, A
72	28	93.3	629	29	US-10-369-493-6887	Sequence 6887, Ap
73	28	93.3	629	32	US-60-360-039-6887	Sequence 6887, Ap
74	27	90.0	6	9	US-08-567-943-3	Sequence 3, Appli



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Query Match 100.0%; Score 30; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVEY 6
Db 1 SVDVEY 6

RESULT 6
US-09-919-703-6
; Sequence 6, Application US/09919703
; GENERAL INFORMATION:
; APPLICANT: Krystal, Gerald
; TITLE OF INVENTION: Peptides and Their Use to Ameliorate
; TITLE OF INVENTION: Cell Death
; FILE REFERENCE: 50216/003004
; CURRENT APPLICATION NUMBER: US/09/919,703
; CURRENT FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: US 09/294,457
; PRIOR FILING DATE: 1999-04-19
; PRIOR APPLICATION NUMBER: US 08/759,599
; PRIOR FILING DATE: 1996-12-05
; PRIOR APPLICATION NUMBER: US 60/008,233
; PRIOR FILING DATE: 1995-12-06
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic polypeptide
US-09-919-703-6

Query Match 100.0%; Score 30; DB 24; Length 20;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVEY 6
Db 1 SVDVEY 6

RESULT 7
US-08-567-943-7
; Sequence 7, Application US/08567943
; GENERAL INFORMATION:
; APPLICANT: Rabkin, Simon W.
; APPLICANT: Krystal, Gerald
; TITLE OF INVENTION: NOVEL PEPTIDES AND THEIR USE TO
; TITLE OF INVENTION: AMELIORATE CELL DEATH
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/567,943
; FILING DATE: 06-DEC-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 780059.401A1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; TELEX: 3723836
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-567-943-6

Query Match 100.0%; Score 30; DB 9; Length 18;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVEY 6
Db 1 SVDVEY 6

RESULT 5
US-08-567-943-6
; Sequence 6, Application US/08567943
; GENERAL INFORMATION:
; APPLICANT: Rabkin, Simon W.
; APPLICANT: Krystal, Gerald
; TITLE OF INVENTION: NOVEL PEPTIDES AND THEIR USE TO
; TITLE OF INVENTION: AMELIORATE CELL DEATH
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/567,943
; FILING DATE: 06-DEC-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 780059.401A1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; TELEX: 3723836
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-567-943-6

```

; REFERENCE/DOCKET NUMBER: 780059.401A1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 622-4900  
; TELEFAX: (206) 682-6031  
; TELEX: 3723836  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 21 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; US-08-567-943-7

Query Match 100.0%; Score 30; DB 9; Length 21;  
Best Local Similarity 100.0%; Pred. No. 13;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVEY 6  
| | | | |  
Db 1 SVDVEY 6

## RESULT 8

US-09-919-703-7  
; Sequence 7, Application US/09919703  
; GENERAL INFORMATION:  
; APPLICANT: Krystal, Gerald  
; APPLICANT: Rakkin, Simon W.  
; TITLE OF INVENTION: Peptides and Their Use to Ameliorate  
; TITLE OF INVENTION: Cell Death  
; FILE REFERENCE: 50216/003004  
; CURRENT APPLICATION NUMBER: US/09/919,703  
; CURRENT FILING DATE: 2001-07-31  
; PRIOR APPLICATION NUMBER: US 09/294,457  
; PRIOR FILING DATE: 1999-04-19  
; PRIOR APPLICATION NUMBER: US 08/759,599  
; PRIOR FILING DATE: 1996-12-05  
; PRIOR APPLICATION NUMBER: US 60/008,233  
; PRIOR FILING DATE: 1995-12-06  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 7  
; LENGTH: 21  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic polypeptide  
; US-09-919-703-7

Query Match 100.0%; Score 30; DB 24; Length 21;  
Best Local Similarity 100.0%; Pred. No. 13;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVEY 6  
| | | | |  
Db 1 SVDVEY 6

## RESULT 9

US-09-791-537-83460  
; Sequence 83460, Application US/09791537  
; GENERAL INFORMATION:  
; APPLICANT: Bionomix, Inc.  
; APPLICANT: Debe, Derek  
; APPLICANT: Danzer, Joseph  
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS  
; TITLE OF INVENTION: METHODS OF USE THEREOF  
; FILE REFERENCE: 261/210  
; CURRENT APPLICATION NUMBER: US/09/791,537  
; CURRENT FILING DATE: 2001-02-22  
; NUMBER OF SEQ ID NOS: 153055  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 83460

; LENGTH: 128  
; TYPE: PRT  
; ORGANISM: Streptococcus pyogenes  
; US-09-791-537-83460

Query Match 100.0%; Score 30; DB 22; Length 128;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVEY 6  
| | | | |  
Db 17 SVDVEY 22

## RESULT 10

US-09-791-537-12562  
; Sequence 12562, Application US/09791537  
; GENERAL INFORMATION:  
; APPLICANT: Bionomix, Inc.  
; APPLICANT: Debe, Derek  
; APPLICANT: Danzer, Joseph  
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS  
; TITLE OF INVENTION: METHODS OF USE THEREOF  
; FILE REFERENCE: 261/210  
; CURRENT APPLICATION NUMBER: US/09/791,537  
; CURRENT FILING DATE: 2001-02-22  
; NUMBER OF SEQ ID NOS: 153055  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 12562  
; LENGTH: 137  
; TYPE: PRT  
; ORGANISM: pdb 1C4PA  
; US-09-791-537-12562

Query Match 100.0%; Score 30; DB 22; Length 137;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVEY 6  
| | | | |  
Db 9 SVDVEY 14

## RESULT 11

US-09-791-537-104248  
; Sequence 104248, Application US/09791537  
; GENERAL INFORMATION:  
; APPLICANT: Bionomix, Inc.  
; APPLICANT: Debe, Derek  
; APPLICANT: Danzer, Joseph  
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS  
; TITLE OF INVENTION: METHODS OF USE THEREOF  
; FILE REFERENCE: 261/210  
; CURRENT APPLICATION NUMBER: US/09/791,537  
; CURRENT FILING DATE: 2001-02-22  
; NUMBER OF SEQ ID NOS: 153055  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 104248  
; LENGTH: 138  
; TYPE: PRT  
; ORGANISM: pdb 1QORA  
; US-09-791-537-104248

Query Match 100.0%; Score 30; DB 22; Length 138;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVEY 6  
| | | | |  
Db 7 SVDVEY 12

## RESULT 12

```
US-09-791-537-23287
; Sequence 23287, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 23287
; LENGTH: 362
; TYPE: PRT
; ORGANISM: pdb 1BMLC
US-09-791-537-23287

Query Match      100.0%; Score 30; DB 22; Length 362;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVDVEY 6
Db 146 SVDVEY 151

RESULT 13
US-09-658-681-3
; Sequence 3, Application US/09658681
; GENERAL INFORMATION:
; APPLICANT: Madrazo, Isis Del Carmen Torrens
; APPLICANT: Garcia, Jose De Jesus De La Fuente
; APPLICANT: Ojalvo, Ariana Garcia
; APPLICANT: Menendez, Alina Seralena
; APPLICANT: Escalona, Elder Pupo
; APPLICANT: Masso, Julio Raul Fernandez
; APPLICANT: Griego, Martha De Jesus Gonzalez
; TITLE OF INVENTION: STREPTOKINASE MUTANTS
; FILE REFERENCE: Sequence Listings 1-14 re: 976-5
; CURRENT APPLICATION NUMBER: US/09/658,681
; CURRENT FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 372
; TYPE: PRT
; ORGANISM: Streptococcus equisimilis
US-09-658-681-3

Query Match      100.0%; Score 30; DB 20; Length 372;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVDVEY 6
Db 157 SVDVEY 162

RESULT 14
US-09-658-681-4
; Sequence 4, Application US/09658681
; GENERAL INFORMATION:
; APPLICANT: Madrazo, Isis Del Carmen Torrens
; APPLICANT: Garcia, Jose De Jesus De La Fuente
; APPLICANT: Ojalvo, Ariana Garcia
; APPLICANT: Menendez, Alina Seralena
; APPLICANT: Escalona, Elder Pupo
; APPLICANT: Masso, Julio Raul Fernandez
; APPLICANT: Griego, Martha De Jesus Gonzalez
; TITLE OF INVENTION: STREPTOKINASE MUTANTS
; FILE REFERENCE: Sequence Listings 1-14 re: 976-5

US-09-791-537-23287
; Sequence 23287, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 23287
; LENGTH: 362
; TYPE: PRT
; ORGANISM: Streptococcus equisimilis
US-09-658-681-4

Query Match      100.0%; Score 30; DB 20; Length 384;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVDVEY 6
Db 157 SVDVEY 162

RESULT 15
US-09-658-681-1
; Sequence 1, Application US/09658681
; GENERAL INFORMATION:
; APPLICANT: Madrazo, Isis Del Carmen Torrens
; APPLICANT: Garcia, Jose De Jesus De La Fuente
; APPLICANT: Ojalvo, Ariana Garcia
; APPLICANT: Menendez, Alina Seralena
; APPLICANT: Escalona, Elder Pupo
; APPLICANT: Masso, Julio Raul Fernandez
; APPLICANT: Griego, Martha De Jesus Gonzalez
; TITLE OF INVENTION: STREPTOKINASE MUTANTS
; FILE REFERENCE: Sequence Listings 1-14 re: 976-5
; CURRENT APPLICATION NUMBER: US/09/658,681
; CURRENT FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 401
; TYPE: PRT
; ORGANISM: Streptococcus equisimilis
US-09-658-681-1

Query Match      100.0%; Score 30; DB 20; Length 401;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVDVEY 6
Db 144 SVDVEY 149

RESULT 16
US-08-567-943-12
; Sequence 12, Application US/08567943
; GENERAL INFORMATION:
; APPLICANT: Rabkin, Simon W.
; APPLICANT: Krystal, Gerald
; TITLE OF INVENTION: NOVEL PEPTIDES AND THEIR USE TO
; TITLE OF INVENTION: AMELIORATE CELL DEATH
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
```

; APPLICATION NUMBER: US/08/567,943  
; FILING DATE: 06-DEC-1995  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mcmasters, David D.  
; REGISTRATION NUMBER: 33,963  
; REFERENCE/DOCKET NUMBER: 780059.401A1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 622-4900  
; TELEFAX: (206) 682-6031  
; TELEX: 3723836  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 413 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-567-943-12

Query Match 100.0%; Score 30; DB 9; Length 413;  
Best Local Similarity 100.0%; Pred. No. 5.4e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVEY 6  
|||||  
Db 156 SVDVEY 161

## RESULT 17

US-09-658-681-2  
; Sequence 2, Application US/09658681  
; GENERAL INFORMATION:  
; APPLICANT: Madrazo, Isis Del Carmen Tortens  
; APPLICANT: Garcia, Jose De Jesus De La Fuente  
; APPLICANT: Ojalvo, Ariana Garcia  
; APPLICANT: Menendez, Alina Seralena  
; APPLICANT: Escalona, Elder Pupo  
; APPLICANT: Masso, Julio Raul Fernandez  
; APPLICANT: Griego, Martha De Jesus Gonzalez  
; TITLE OF INVENTION: STREPTOKINASE MUTANTS  
; FILE REFERENCE: Sequence Listings 1-14 re: 976-5  
; CURRENT APPLICATION NUMBER: US/09/658,681  
; CURRENT FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 413  
; TYPE: PRT  
; ORGANISM: Streptococcus equisimilis  
US-09-658-681-2

Query Match 100.0%; Score 30; DB 20; Length 413;  
Best Local Similarity 100.0%; Pred. No. 5.4e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVEY 6  
|||||  
Db 144 SVDVEY 149

## RESULT 18

US-09-919-703-12  
; Sequence 12, Application US/09919703  
; GENERAL INFORMATION:  
; APPLICANT: Krystal, Gerald  
; APPLICANT: Rabkin, Simon W.  
; TITLE OF INVENTION: Peptides and Their Use to Ameliorate  
; TITLE OF INVENTION: Cell Death  
; FILE REFERENCE: 50216/003004  
; CURRENT APPLICATION NUMBER: US/09/919,703  
; CURRENT FILING DATE: 2001-07-31  
; PRIOR APPLICATION NUMBER: US 09/294,457  
; PRIOR FILING DATE: 1999-04-19

; PRIOR APPLICATION NUMBER: US 08/759,599  
; PRIOR FILING DATE: 1996-12-05  
; PRIOR APPLICATION NUMBER: US 60/008,233  
; PRIOR FILING DATE: 1995-12-06  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 12  
; LENGTH: 413  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic polypeptide  
US-09-919-703-12

Query Match 100.0%; Score 30; DB 24; Length 413;  
Best Local Similarity 100.0%; Pred. No. 5.4e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVEY 6  
|||||  
Db 156 SVDVEY 161

## RESULT 19

US-10-360-101-264  
; Sequence 264, Application US/10360101  
; GENERAL INFORMATION:  
; APPLICANT: Moll, Gert N.  
; APPLICANT: Leenhouts, Cornelis J.  
; TITLE OF INVENTION: Export and modification of (poly)peptide in the lantibiotic way  
; FILE REFERENCE: 2183-5673  
; CURRENT APPLICATION NUMBER: US/10/360,101  
; CURRENT FILING DATE: 2003-02-07  
; PRIOR APPLICATION NUMBER: EP 02077050.8  
; PRIOR FILING DATE: 2002-05-24  
; NUMBER OF SEQ ID NOS: 309  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 264  
; LENGTH: 413  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: sequence of streptokinase  
US-10-360-101-264

Query Match 100.0%; Score 30; DB 29; Length 413;  
Best Local Similarity 100.0%; Pred. No. 5.4e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVEY 6  
|||||  
Db 157 SVDVEY 162

## RESULT 20

PCT-US93-09502-1  
; Sequence 1, Application PC/TUS9309502  
; GENERAL INFORMATION:  
; APPLICANT: Reed, Guy L.  
; TITLE OF INVENTION: Peptides Specifically Binding to Plasminogen And the  
; TITLE OF INVENTION: DNA Encoding Such Peptides  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sterne, Kessler, Goldstein and Fox  
; STREET: 1100 New York Avenue, Suite 600  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS



SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/09502  
FILING DATE: Herewith  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Sanzo, Michael A.  
REGISTRATION NUMBER: 36,912  
REFERENCE/DOCKET NUMBER: 0609.3570001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 371-2600  
TELEFAX: (202) 371-2545  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 414 amino acids  
TYPE: amino acid  
STRANDEDNESS: both  
TOPOLOGY: both  
PCT-US93-09502-1

Query Match 100.0%; Score 30; DB 1; Length 414;  
Best Local Similarity 100.0%; Pred. No. 5.4e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVEY 6  
DB 157 SVDVEY 162

RESULT 21  
US-07-956-692A-9  
SEQUENCE 9, Application US/07956692A  
GENERAL INFORMATION:  
APPLICANT: Reed, Guy L.  
APPLICANT: Kussie, Paul  
APPLICANT: Parhami-Seren, Behnaz  
TITLE OF INVENTION: Recombinant Streptokinase Fragments with  
TITLE OF INVENTION: Decreased Antigenicity and Uses Thereof  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sterne, Kessler, Goldstein and Fox  
STREET: 1225 Connecticut Avenue  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/956,692A  
FILING DATE: 19921005  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Goldstein, Jorge A.  
REGISTRATION NUMBER: 29,021  
REFERENCE/DOCKET NUMBER: 0609.3570000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 833-7533  
TELEFAX: (202) 833-8716  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 414 amino acids  
TYPE: AMINO ACID  
STRANDEDNESS: both  
TOPOLOGY: both  
US-07-956-692A-9

Query Match 100.0%; Score 30; DB 3; Length 414;  
Best Local Similarity 100.0%; Pred. No. 5.4e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVEY 6  
DB 157 SVDVEY 162

RESULT 22  
US-08-128-299-1  
SEQUENCE 1, Application US/08128299  
GENERAL INFORMATION:  
APPLICANT: Reed, Guy L.  
TITLE OF INVENTION: Peptides Specifically Binding to Plasminogen And the  
TITLE OF INVENTION: DNA Encoding Such Peptides  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sterne, Kessler, Goldstein and Fox  
STREET: 1100 New York Avenue, Suite 600  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/128,299  
FILING DATE: Herewith  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Sanzo, Michael A.  
REGISTRATION NUMBER: 36,912  
REFERENCE/DOCKET NUMBER: 0609.3570001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 371-2600  
TELEFAX: (202) 371-2545  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 414 amino acids  
TYPE: amino acid  
STRANDEDNESS: both  
TOPOLOGY: both  
US-08-128-299-1

Query Match 100.0%; Score 30; DB 5; Length 414;  
Best Local Similarity 100.0%; Pred. No. 5.4e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVEY 6  
DB 157 SVDVEY 162

RESULT 23  
US-09-438-136-252  
SEQUENCE 252, Application US/09438136  
GENERAL INFORMATION:  
APPLICANT: CARR, Francis Joseph  
ADAIR, Fiona Suzanne  
HAMILTON, Anita Anne  
CARTER, Graham  
TITLE OF INVENTION: METHOD FOR THE PRODUCTION OF  
NON-IMMUNOGENIC PROTEINS  
NUMBER OF SEQUENCES: 254  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hale and Dorr L.L.P.  
STREET: 60 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: United States  
ZIP: 02109  
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/438,136  
FILING DATE: 10-Nov-1999  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/GB98/01473  
FILING DATE: 21-MAY-1998  
APPLICATION NUMBER: GB 9710480.6  
FILING DATE: 21-MAY-1997  
APPLICATION NUMBER: GB 9716197.0  
FILING DATE: 31-JUL-1997  
APPLICATION NUMBER: GB 9725270.4  
FILING DATE: 28-NOV-1997  
APPLICATION NUMBER: GB 9807751.4  
FILING DATE: 14-APR-1998  
APPLICATION NUMBER: US 60/067,235  
FILING DATE: 02-DEC-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Baker, Hollie L.  
REGISTRATION NUMBER: 31,321  
REFERENCE/DOCKET NUMBER: 102286.395CON  
TELEPHONE: (617) 526-6000  
INFORMATION FOR SEQ ID NO: 252:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 414 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 252:  
US-09-438-136-252

Query Match 100.0%; Score 30; DB 18; Length 414;  
Best Local Similarity 100.0%; Pred. No. 5.4e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVEY 6  
Db 157 SVDVEY 162

RESULT 24  
US-09-438-136-253  
Sequence 253, Application US/09438136  
GENERAL INFORMATION:  
APPLICANT: CARR, Francis Joseph  
ADAIR, Fiona Suzanne  
HAMILTON, Anita Anne  
CARTER, Graham  
TITLE OF INVENTION: METHOD FOR THE PRODUCTION OF  
NON-IMMUNOGENIC PROTEINS  
NUMBER OF SEQUENCES: 254  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hale and Dorr L.L.P.  
STREET: 60 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: United States  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/438,136  
FILING DATE: 10-Nov-1999  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/GB98/01473

FILING DATE: 21-MAY-1998  
APPLICATION NUMBER: GB 9710480.6  
FILING DATE: 21-MAY-1997  
APPLICATION NUMBER: GB 9716197.0  
FILING DATE: 31-JUL-1997  
APPLICATION NUMBER: GB 9725270.4  
FILING DATE: 28-NOV-1997  
APPLICATION NUMBER: GB 9807751.4  
FILING DATE: 14-APR-1998  
APPLICATION NUMBER: US 60/067,235  
FILING DATE: 02-DEC-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Baker, Hollie L.  
REGISTRATION NUMBER: 31,321  
REFERENCE/DOCKET NUMBER: 102286.395CON  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 526-6000  
INFORMATION FOR SEQ ID NO: 253:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 414 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 253:  
US-09-438-136-253

Query Match 100.0%; Score 30; DB 18; Length 414;  
Best Local Similarity 100.0%; Pred. No. 5.4e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVEY 6  
Db 157 SVDVEY 162

RESULT 25  
US-09-471-349-2  
Sequence 2, Application US/09471349  
GENERAL INFORMATION:  
APPLICANT: Sahni, Girish  
APPLICANT: Kumar, Rajesh  
APPLICANT: Roy, Chaiti  
APPLICANT: Rajagopal, Kammara  
APPLICANT: Nihalani, Deepak  
APPLICANT: Sundaram, Vasudha  
APPLICANT: Yadav, Mahavir  
TITLE OF INVENTION: NOVEL CLOT-SPECIFIC STREPTOKINASE PROTEINS POSSESSING ALTERED  
TITLE OF INVENTION: PLASMINOGEN ACTIVATION CHARACTERISTICS AND A PROCESS FOR THE  
FILE OF INVENTION: PREPARATION OF SAID PROTEINS  
FILE REFERENCE: 07064/009001  
CURRENT APPLICATION NUMBER: US/09/471,349  
CURRENT FILING DATE: 1999-12-23  
PRIOR APPLICATION NUMBER: IN 3825/DEL/98  
PRIOR FILING DATE: 1998-12-24  
NUMBER OF SEQ ID NOS: 24  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 2  
LENGTH: 414  
TYPE: PRT  
ORGANISM: Streptococcus equisimilis  
US-09-471-349-2

Query Match 100.0%; Score 30; DB 18; Length 414;  
Best Local Similarity 100.0%; Pred. No. 5.4e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVEY 6  
Db 157 SVDVEY 162

RESULT 26  
US-09-633-516B-7  
Sequence 7, Application US/09633516B

```
; GENERAL INFORMATION:
; APPLICANT: Francis Joseph CARR
; APPLICANT: Fiona Suzanne ADAIR
; APPLICANT: Anita Anne HAMILTON
; APPLICANT: Graham CARTER
; TITLE OF INVENTION: Modifying Protein Immunogenicity
; FILE REFERENCE: 112408-120
; CURRENT APPLICATION NUMBER: US/09/633.516B
; 2000-08-04
; CURRENT FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: PCT/GB99/04119
; PRIOR FILING DATE: 1999-12-08
; PRIOR APPLICATION NUMBER: GB9826925.1
; PRIOR FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: GB9902139.6
; PRIOR FILING DATE: 1999-02-02
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 414
; TYPE: PRT
; ORGANISM: Streptococcus equisimilis
; US-09-633-516B-7

Query Match      100.0%; Score 30; DB 20; Length 414;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVDVEY 6
Db 157 SVDVEY 162

RESULT 27
US-09-633-516B-8
; Sequence 8, Application US/09633516B
; GENERAL INFORMATION:
; APPLICANT: Francis Joseph CARR
; APPLICANT: Fiona Suzanne ADAIR
; APPLICANT: Anita Anne HAMILTON
; APPLICANT: Graham CARTER
; TITLE OF INVENTION: Modifying Protein Immunogenicity
; FILE REFERENCE: 112408-120
; CURRENT APPLICATION NUMBER: US/09/633.516B
; 2000-08-04
; CURRENT FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: PCT/GB99/04119
; PRIOR FILING DATE: 1999-12-08
; PRIOR APPLICATION NUMBER: GB9826925.1
; PRIOR FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: GB9902139.6
; PRIOR FILING DATE: 1999-02-02
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 414
; TYPE: PRT
; ORGANISM: Streptococcus equisimilis
; US-09-633-516B-8

Query Match      100.0%; Score 30; DB 20; Length 414;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVDVEY 6
Db 157 SVDVEY 162

RESULT 28
US-09-791-537-418
; Sequence 418, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEME
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 418
; LENGTH: 414
; TYPE: PRT
; ORGANISM: Streptococcus equisimilis
; US-09-791-537-418

Query Match      100.0%; Score 30; DB 22; Length 414;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVDVEY 6
Db 157 SVDVEY 162

RESULT 29
US-09-940-235-2
; Sequence 2, Application US/09940235
; GENERAL INFORMATION:
; APPLICANT: Kumar, Rajesh
; APPLICANT: Sahni, Girish
; APPLICANT: Roy, Chait
; APPLICANT: Rajagopal, Kammar
; APPLICANT: Nihalani, Deepak
; APPLICANT: Sundaram, Vasudha
; APPLICANT: Yadav, Mahavir
; TITLE OF INVENTION: NOVEL CLOT-SPECIFIC STREPTOKINASE
; TITLE OF INVENTION: PROTEINS POSSESSING ALTERED PLASMINOGEN ACTIVATION
; TITLE OF INVENTION: CHARACTERISTICS AND A PROCESS FOR THE PREPARATION OF SAID
; TITLE OF INVENTION: PROTEIN
; FILE REFERENCE: 07064-009002
; CURRENT APPLICATION NUMBER: US/09/940,235
; CURRENT FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 09/471,349
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: IN 3825/DEL/98
; PRIOR FILING DATE: 1998-12-24
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 414
; TYPE: PRT
; ORGANISM: Streptococcus equisimilis
; US-09-940-235-2

Query Match      100.0%; Score 30; DB 24; Length 414;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVDVEY 6
Db 157 SVDVEY 162

RESULT 30
US-10-300-215-252
; Sequence 252, Application US/10300215
; GENERAL INFORMATION:
; APPLICANT: Carr, Francis Joseph
; APPLICANT: ADAIR, Fiona Suzanne
; APPLICANT: HAMILTON, Anita Anne
; APPLICANT: CARTER, Graham
; TITLE OF INVENTION: METHOD FOR THE PRODUCTION OF
```

Best Local Similarity 100.0%; Pred. No. 5.4e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVEY 6  
Db 157 SVDVEY 162

RESULT 32  
US-10-631-558-2  
; Sequence 2, Application US/10631558  
; GENERAL INFORMATION:  
; APPLICANT: Kumar, Rajesh  
; APPLICANT: Sahni, Girish  
; APPLICANT: Roy, Chait  
; APPLICANT: Rajagopal, Kamara  
; APPLICANT: Nihalani, Deepak  
; APPLICANT: Sundaram, Vasudha  
; APPLICANT: Yadav, Mahavir  
; TITLE OF INVENTION: NOVEL CLOT-SPECIFIC STREPTOKINASE  
; TITLE OF INVENTION: PROTEINS POSSESSING ALTERED PLASMINOGEN ACTIVATION  
; TITLE OF INVENTION: CHARACTERISTICS AND A PROCESS FOR THE PREPARATION OF SAID  
; FILE OF INVENTION: PROTEIN  
; FILE REFERENCE: 07064-009002  
; CURRENT APPLICATION NUMBER: US/10/631,558  
; CURRENT FILING DATE: 2003-07-31  
; PRIOR APPLICATION NUMBER: US/09/940,235  
; PRIOR FILING DATE: 2002-04-09  
; PRIOR APPLICATION NUMBER: 09/471,349  
; PRIOR FILING DATE: 1999-12-23  
; PRIOR APPLICATION NUMBER: IN 3825/DEL/98  
; PRIOR FILING DATE: 1998-12-24  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 414  
; TYPE: PRT  
; ORGANISM: Streptococcus equisimilis  
US-10-631-558-2

Query Match 100.0%; Score 30; DB 31; Length 414;  
Best Local Similarity 100.0%; Pred. No. 5.4e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVEY 6  
Db 157 SVDVEY 162

RESULT 33  
US-09-305-958-4  
; Sequence 4, Application US/09305958  
; GENERAL INFORMATION:  
; APPLICANT: Zhang, Xuejun C  
; APPLICANT: Lin, Xinli  
; APPLICANT: Tang, Jordan  
; TITLE OF INVENTION: Thrombolytic Agents Derived from Streptokinase  
; FILE REFERENCE: OMRF 173  
; CURRENT APPLICATION NUMBER: US/09/305,958  
; CURRENT FILING DATE: 1999-05-06  
; EARLIER APPLICATION NUMBER: 60/084,392  
; EARLIER FILING DATE: 1998-05-06  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 4  
; LENGTH: 415  
; TYPE: PRT  
; ORGANISM: Streptococcus sp.  
; FEATURE:  
; NAME/KEY: PEPTIDE  
; LOCATION: (1)..(415)  
; OTHER INFORMATION: streptokinase  
US-09-305-958-4

Best Local Similarity 100.0%; Pred. No. 5.4e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVEY 6  
Db 157 SVDVEY 162

RESULT 31  
US-10-300-215-253  
; Sequence 253, Application US/10300215  
; GENERAL INFORMATION:  
; APPLICANT: CARR, Francis Joseph  
; APPLICANT: ADAIR, Fiona Suzanne  
; APPLICANT: HAMILTON, Anita Anne  
; APPLICANT: CARTER, Graham  
; TITLE OF INVENTION: METHOD FOR THE PRODUCTION OF  
; TITLE OF INVENTION: NON-IMMUNOGENIC PROTEINS  
; FILE REFERENCE: MER-104-Con.1  
; CURRENT APPLICATION NUMBER: US/10/300,215  
; CURRENT FILING DATE: 2002-11-20  
; PRIOR APPLICATION NUMBER: US 09/438,136  
; PRIOR FILING DATE: 1999-11-10  
; PRIOR APPLICATION NUMBER: WO PCT/GB98/01473  
; PRIOR FILING DATE: 1998-05-21  
; PRIOR APPLICATION NUMBER: GB 9710480.6  
; PRIOR FILING DATE: 1997-07-31  
; PRIOR APPLICATION NUMBER: GB 9725270.4  
; PRIOR FILING DATE: 1997-11-28  
; PRIOR APPLICATION NUMBER: GB 9807751.4  
; PRIOR FILING DATE: 1998-04-14  
; PRIOR APPLICATION NUMBER: US 60/067,235  
; PRIOR FILING DATE: 1997-12-02  
; NUMBER OF SEQ ID NOS: 254  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 252  
; LENGTH: 414  
; TYPE: PRT  
; ORGANISM: Streptococcus equisimilis  
US-10-300-215-252

Query Match 100.0%; Score 30; DB 29; Length 414;  
Best Local Similarity 100.0%; Pred. No. 5.4e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVEY 6  
Db 157 SVDVEY 162

RESULT 32  
US-10-300-215-252  
; Sequence 253, Application US/10300215  
; GENERAL INFORMATION:  
; APPLICANT: CARR, Francis Joseph  
; APPLICANT: ADAIR, Fiona Suzanne  
; APPLICANT: HAMILTON, Anita Anne  
; APPLICANT: CARTER, Graham  
; TITLE OF INVENTION: METHOD FOR THE PRODUCTION OF  
; TITLE OF INVENTION: NON-IMMUNOGENIC PROTEINS  
; FILE REFERENCE: MER-104-Con.1  
; CURRENT APPLICATION NUMBER: US/10/300,215  
; CURRENT FILING DATE: 2002-11-20  
; PRIOR APPLICATION NUMBER: US 09/438,136  
; PRIOR FILING DATE: 1999-11-10  
; PRIOR APPLICATION NUMBER: WO PCT/GB98/01473  
; PRIOR FILING DATE: 1998-05-21  
; PRIOR APPLICATION NUMBER: GB 9710480.6  
; PRIOR FILING DATE: 1997-07-31  
; PRIOR APPLICATION NUMBER: GB 9725270.4  
; PRIOR FILING DATE: 1997-11-28  
; PRIOR APPLICATION NUMBER: GB 9807751.4  
; PRIOR FILING DATE: 1998-04-14  
; PRIOR APPLICATION NUMBER: US 60/067,235  
; PRIOR FILING DATE: 1997-12-02  
; NUMBER OF SEQ ID NOS: 254  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 253  
; LENGTH: 414  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Modified strep protein  
US-10-300-215-253

Query Match 100.0%; Score 30; DB 29; Length 414;

```
Query Match      100.0%; Score 30; DB 17; Length 415;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVDVEY 6
    |||||
Db 157 SVDVEY 162

RESULT 34
US-09-305-970-5
; Sequence 5, Application US/09305970
; GENERAL INFORMATION:
; APPLICANT: Lin, Xinli
; APPLICANT: Zhang, Xuejun C
; APPLICANT: Tang, Jordan
; TITLE OF INVENTION: Human Plasminogen Activator
; FILE REFERENCE: OMRF 175
; CURRENT APPLICATION NUMBER: US/09/305.970
; CURRENT FILING DATE: 1999-05-06
; EARLIER APPLICATION NUMBER: 60/110,588
; EARLIER FILING DATE: 1998-12-02
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 415
; TYPE: PRT
; ORGANISM: Streptococcus sp.
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(415)
; OTHER INFORMATION: streptokinase
;
US-09-305-970-5

Query Match      100.0%; Score 30; DB 17; Length 415;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVDVEY 6
    |||||
Db 157 SVDVEY 162

RESULT 35
US-09-791-537-32688
; Sequence 32688, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMB
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791.537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 32688
; LENGTH: 415
; TYPE: PRT
; ORGANISM: Streptococcus equisimilis
;
US-09-791-537-32688

Query Match      100.0%; Score 30; DB 22; Length 440;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVDVEY 6
    |||||
Db 158 SVDVEY 163

RESULT 36
US-09-791-537-45187
; Sequence 45187, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMB
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791.537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 45187
; LENGTH: 440
; TYPE: PRT
; ORGANISM: Streptococcus equisimilis
;
US-09-791-537-45187

Query Match      100.0%; Score 30; DB 22; Length 440;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVDVEY 6
    |||||
Db 183 SVDVEY 188

RESULT 37
US-09-791-537-45189
; Sequence 45189, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMB
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791.537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 45189
; LENGTH: 440
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
;
US-09-791-537-45189

Query Match      100.0%; Score 30; DB 22; Length 440;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVDVEY 6
    |||||
Db 183 SVDVEY 188

RESULT 38
US-09-791-537-45192
; Sequence 45192, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMB
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791.537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 45192
```

LENGTH: 440  
TYPE: PRT  
ORGANISM: Streptococcus sp  
US-09-791-537-45192

Query Match 100.0%; Score 30; DB 22; Length 440;  
Best Local Similarity 100.0%; Pred. No. 5.9e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVEY 6  
Db 183 SVDVEY 188

RESULT 39  
US-09-609-360B-25  
Sequence 25, Application US/09609360B  
GENERAL INFORMATION:  
APPLICANT: Hodge, Martin R.  
APPLICANT: Meyers, Rachel  
APPLICANT: Williamson, Mark  
TITLE OF INVENTION: Novel Kinases and Uses Thereof  
FILE REFERENCE: 35800/200938  
CURRENT APPLICATION NUMBER: US/09/609,360B  
PRIOR FILING DATE: 2000-11-13  
PRIOR APPLICATION NUMBER: US 09/345,473  
PRIOR FILING DATE: 1999-06-30  
PRIOR APPLICATION NUMBER: US 09/562,480  
PRIOR FILING DATE: 2000-05-01  
NUMBER OF SEQ ID NOS: 83  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 25  
LENGTH: 891  
TYPE: PRT  
ORGANISM: Hydra vulgaris  
US-09-609-360B-25

Query Match 100.0%; Score 30; DB 20; Length 891;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVEY 6  
Db 137 SVDVEY 142

RESULT 40  
US-09-609-360C-25  
Sequence 25, Application US/09609360C  
GENERAL INFORMATION:  
APPLICANT: Hodge, Martin R.  
APPLICANT: Meyers, Rachel  
APPLICANT: Williamson, Mark  
TITLE OF INVENTION: Novel Kinases and Uses Thereof  
FILE REFERENCE: MPI1999-096CP2  
CURRENT APPLICATION NUMBER: US/09/609,360C  
CURRENT FILING DATE: 2000-06-30  
PRIOR APPLICATION NUMBER: 09/562,480  
PRIOR FILING DATE: 2000-05-01  
PRIOR APPLICATION NUMBER: 09/345,473  
PRIOR FILING DATE: 1999-06-30  
NUMBER OF SEQ ID NOS: 83  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 25  
LENGTH: 891  
TYPE: PRT  
ORGANISM: Hydra vulgaris  
US-09-609-360C-25

Query Match 100.0%; Score 30; DB 20; Length 891;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVEY 6  
Db 137 SVDVEY 142

RESULT 41  
US-09-609-360D-25  
Sequence 25, Application US/09609360D  
GENERAL INFORMATION:  
APPLICANT: Hodge, Martin R.  
APPLICANT: Meyers, Rachel  
APPLICANT: Williamson, Mark  
TITLE OF INVENTION: Novel Kinases and Uses Thereof  
FILE REFERENCE: MPI1999-096CP2  
CURRENT APPLICATION NUMBER: US/09/609,360D  
CURRENT FILING DATE: 2000-06-30  
PRIOR APPLICATION NUMBER: 09/562,480  
PRIOR FILING DATE: 2000-05-01  
PRIOR APPLICATION NUMBER: 09/345,473  
PRIOR FILING DATE: 1999-06-30  
NUMBER OF SEQ ID NOS: 90  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 25  
LENGTH: 891  
TYPE: PRT  
ORGANISM: Hydra vulgaris  
US-09-609-360D-25

Query Match 100.0%; Score 30; DB 20; Length 891;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVEY 6  
Db 137 SVDVEY 142

RESULT 42  
US-09-791-537-145994  
Sequence 145994, Application US/09791537  
GENERAL INFORMATION:  
APPLICANT: Bionomix, Inc.  
APPLICANT: Debe, Derek  
APPLICANT: Danzer, Joseph  
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMB  
METHODS OF USE THEREOF  
FILE REFERENCE: 261/210  
CURRENT APPLICATION NUMBER: US/09/791,537  
CURRENT FILING DATE: 2001-02-22  
NUMBER OF SEQ ID NOS: 153055  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 145994  
LENGTH: 891  
TYPE: PRT  
ORGANISM: Hydra vulgaris  
US-09-791-537-145994

Query Match 100.0%; Score 30; DB 22; Length 891;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVEY 6  
Db 137 SVDVEY 142

RESULT 43  
US-09-862-027-25  
Sequence 25, Application US/09862027  
GENERAL INFORMATION:  
APPLICANT: Hodge, Martin R.  
TITLE OF INVENTION: Novel Kinases and Uses Thereof  
FILE REFERENCE: 35800/234862

Query Match	Score	DB	Length	DB 32	Length 43
Best Local Similarity	96.7%	Score 29	DB 32	Length 43	
Matches	5	Conservative	1	Mismatches	0
Indels	0	Gaps	0		
QY	1	SVDVEY 6			
DB	35	SIDVEY 40			
RESULT 46					
US-60-143-753-234					
Sequence 234	Application US/60143753				
GENERAL INFORMATION:					
APPLICANT:	Kerlavage, Anthony				
TITLE OF INVENTION:	ISOLATED ION CHANNEL PROTEINS, NUCLEIC				
TITLE OF INVENTION:	ACID MOLECULES ENCODING ION CHANNEL PROTEINS, AND USES				
TITLE OF INVENTION:	THEREOF				
FILE REFERENCE:	CL000046				
CURRENT APPLICATION NUMBER:	US/60/143,753				
CURRENT FILING DATE:	1999-07-01				
NUMBER OF SEQ ID NOS:	461				
SOFTWARE:	FastSeq for Windows Version 3.0				
SEQ ID NO 234					
LENGTH:	43				
TYPE:	PRT				
ORGANISM:	Drosophila				
FEATURE:					
NAME/KEY:	VARIANT				
LOCATION:	(1)...(43)				
OTHER INFORMATION:	Xaa = Any Amino Acid				
US-60-143-753-234					
Query Match	96.7%	Score 29	DB 32	Length 43	
Best Local Similarity	83.3%	Pred. No. 56			
Matches	5	Conservative	1	Mismatches	0
Indels	0	Gaps	0		
QY	1	SVDVEY 6			
DB	35	SIDVEY 40			
RESULT 47					
US-60-145-989-236					
Sequence 236	Application US/60145989				
GENERAL INFORMATION:					
APPLICANT:	Bonazzi, Vivien				
TITLE OF INVENTION:	ISOLATED ION CHANNEL PROTEINS, NUCLEIC				
TITLE OF INVENTION:	ACID MOLECULES ENCODING ION CHANNEL PROTEINS, AND USES				
TITLE OF INVENTION:	THEREOF				
FILE REFERENCE:	CL000066				
CURRENT APPLICATION NUMBER:	US/60/145,989				
CURRENT FILING DATE:	1999-07-29				
NUMBER OF SEQ ID NOS:	456				
SOFTWARE:	FastSeq for Windows Version 3.0				
SEQ ID NO 236					
LENGTH:	66				
TYPE:	PRT				
ORGANISM:	Drosophila				
FEATURE:					
NAME/KEY:	VARIANT				
LOCATION:	(1)...(66)				
OTHER INFORMATION:	Xaa = Any Amino Acid				
US-60-145-989-236					
Query Match	96.7%	Score 29	DB 32	Length 66	
Best Local Similarity	83.3%	Pred. No. 96			
Matches	5	Conservative	1	Mismatches	0
Indels	0	Gaps	0		
QY	1	SVDVEY 6			
DB	35	SIDVEY 40			

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RESULT 48
US-60-145-138-515
; Sequence 515 Application US/60145138
; GENERAL INFORMATION:
; APPLICANT: Bonazzi, Vivien
; TITLE OF INVENTION: ISOLATED SECRETED PROTEINS, NUCLEIC ACID
; FILE REFERENCE: CLO00062
; CURRENT APPLICATION NUMBER: US/60/145,138
; CURRENT FILING DATE: 1999-07-22
; NUMBER OF SEQ ID NOS: 948
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 515
; LENGTH: 68
; TYPE: PRT
; ORGANISM: Drosophila
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(68)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-60-145-138-515

Query Match          96.7%; Score 29; DB 32; Length 68;
Best Local Similarity 83.3%; Pred. No. 1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 SVDVEY 6
Db      38 SIDVEY 43

RESULT 49
US-60-145-989-317
; Sequence 317, Application US/60145989
; GENERAL INFORMATION:
; APPLICANT: Bonazzi, Vivien
; TITLE OF INVENTION: ISOLATED ION CHANNEL PROTEINS, NUCLEIC
; FILE REFERENCE: CLO00066
; CURRENT APPLICATION NUMBER: US/60/145,989
; CURRENT FILING DATE: 1999-07-29
; NUMBER OF SEQ ID NOS: 456
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 317
; LENGTH: 68
; TYPE: PRT
; ORGANISM: Drosophila
US-60-145-989-317

Query Match          96.7%; Score 29; DB 32; Length 68;
Best Local Similarity 83.3%; Pred. No. 1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 SVDVEY 6
Db      38 SIDVEY 43

RESULT 50
US-10-424-599-271681
; Sequence 271681, Application US/10424599
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
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; SEQ ID NO 271681
; LENGTH: 72
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(72)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_87347C.1.pep
US-10-424-599-271681

Query Match          96.7%; Score 29; DB 30; Length 72;
Best Local Similarity 83.3%; Pred. No. 1.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 SVDVEY 6
Db      19 SIDVEY 24

Search completed: January 20, 2004, 14:01:20
Job time : 174 secs
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 20, 2004, 14:37:25 ; Search time 42 Seconds  
(without alignments)  
22.675 Million cell updates/sec

Title: US-09-919-703-1

Perfect score: 30

Sequence: 1 SVDVEY 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 75 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	30	100.0	6	20	AA25009
2	30	100.0	6	23	AB80001
3	30	100.0	16	23	AB80005
4	30	100.0	18	20	AA25013
5	30	100.0	20	20	AA25014
6	30	100.0	20	23	AB80006
7	30	100.0	20	24	ABG76052
8	30	100.0	21	20	AA25015
9	30	100.0	21	23	AB80007
10	30	100.0	21	23	AB80007
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12	30	100.0	21	23	AB80007
13	30	100.0	21	23	AB80007
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32	30	100.0	21	23	AB80007
33	30	100.0	21	23	AB80007
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11	30	100.0	146	20	AA2501558
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17	30	100.0	369	12	AA2501556
18	30	100.0	371	12	AA2501556
19	30	100.0	372	12	AA2501556
20	30	100.0	372	12	AA2501556
21	30	100.0	372	12	AA2501556
22	30	100.0	374	12	AA2501556
23	30	100.0	384	21	AA2501556
24	30	100.0	384	21	AA2501556
25	30	100.0	391	12	AA2501556
26	30	100.0	401	21	AA2501556
27	30	100.0	413	20	AA2501556
28	30	100.0	413	20	AA2501556
29	30	100.0	413	20	AA2501556
30	30	100.0	414	12	AA2501556
31	30	100.0	414	12	AA2501556
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33	30	100.0	414	12	AA2501556
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70	30	100.0	414	12	AA2501556
71	30	100.0	414	12	AA2501556
72	30	100.0	414	12	AA2501556
73	30	100.0	414	12	AA2501556
74	30	100.0	414	12	AA2501556
75	30	100.0	414	12	AA2501556

ALIGNMENTS

RESULT 1  
AA25009

ID AAY25009 standard; peptide; 6 AA.  
 AC AAY25009;  
 XX  
 DT 23-AUG-1999 (first entry)  
 XX  
 DE Streptokinase derived peptide 1 for amelioration of cell death.  
 XX  
 KW Streptokinase; cell death; amelioration; treatment; disease; aging; AIDS;  
 KW cellular differentiation; physical insult; trauma; anoxia; hyperthermia;  
 KW hypothermia; brain; spinal cord; kidney; heart; lung; liver; skin; HIV;  
 KW viral disorder; hepatitis; retroviral; infection; encephalitis; FALS;  
 KW neurodegenerative disorder; Parkinson's disease; Alzheimer's disease;  
 KW Huntington's disease; cerebellar degeneration; cardiovascular disease;  
 KW familial amyotrophic lateral sclerosis; atherosclerosis; heart failure;  
 KW infarction; heart disease; cardiomyopathy; hypertensive; myocardial;  
 KW reperfusion injury; immune disease; rheumatoid arthritis; renal; retinal;  
 KW systemic lupus erythematosus; insulin-dependent; diabetes mellitus;  
 KW pernicious anaemia; dermatomyositis; erythema nodosum; myasthenia gravis;  
 KW Sjogren's syndrome; temporal arthritis; autoimmune polyarthritis;  
 KW Wegener's granulomatosis; glomerulonephritis; anti-phospholipid syndrome;  
 KW neoplastic disorder; leukemia; sarcoma; myeloma; carcinoma; neuroma;  
 KW melanoma; cancer; breast; colon; cervix; prostate; Hodgkin's disease;  
 KW non-Hodgkin's lymphoma; inflammatory disorder; stroke; ischemia;  
 KW spinal cord; toxic insult; pulmonary; macular degeneration; cataract;  
 KW pancreatitis; Crohn's disease; ulcerative colitis; motor neuron disease;  
 KW Guillan Barre Syndrome; demyelinating disease; bypass surgery;  
 KW chemotherapy; clozapine; AZT; anthracycline.  
 XX  
 OS Synthetic.  
 XX  
 PN US5917013-A.  
 XX  
 PD 29-JUN-1999.  
 XX  
 PF 05-DEC-1996; 96US-0759599.  
 XX  
 PR 06-DEC-1995; 95US-0008233.  
 PR 05-DEC-1996; 96US-0759599.  
 XX  
 PA (RABK/) RABKIN S W.  
 XX  
 PI Krystal G, Rabkin SW;  
 XX  
 DR WPI; 1999-394231/33.  
 XX  
 PT Peptides that ameliorate cell death useful for treating conditions  
 PT associated with cellular differentiation  
 XX  
 PS Claim 2; Column 12; 15pp; English.  
 XX  
 CC AAY25009-Y25019 are novel peptides derived from streptokinase that  
 CC ameliorate cell death. The products of the invention and their encoding  
 CC nucleic acids may be useful for treating diseases and conditions related  
 CC to aging, cellular differentiation, physical insult (e.g. physical  
 CC trauma, anoxia, hyperthermia, hypothermia, chemically induced damage,  
 CC and trauma to the brain, spinal cord, kidney, heart, lungs, liver, skin  
 CC and any other organ), viral disorders (e.g. hepatitis, retroviral  
 CC infections, viral encephalitis, and AIDS/HIV), neurodegenerative  
 CC disorders (e.g. Parkinson's disease, Alzheimer's disease, Huntington's  
 CC disease, cerebellar degenerations, and familial amyotrophic lateral  
 CC sclerosis (FALS)), cardiovascular disease (e.g. atherosclerosis,  
 CC myocardial infarction, heart failure, cardiomyopathy, myocardial  
 CC reperfusion injury, and hypertensive heart disease), immune disease (e.g.  
 CC rheumatoid arthritis, systemic lupus erythematosus, insulin-dependent,  
 CC diabetes mellitus, lupus, pernicious anaemia, dermatomyositis, erythema  
 CC nodosum, Sjogren's syndrome, temporal arthritis, myasthenia gravis,  
 CC Wegener's granulomatosis, glomerulonephritis, anti-phospholipid syndrome,  
 CC and autoimmune polyarthritis), a neoplastic disorder (e.g. leukemia,  
 CC sarcomas, myelomas, carcinomas, neuromas, melanoma, cancers of the  
 CC breast, brain, colon, cervix, and prostate, Hodgkin's disease and  
 CC non-Hodgkin's lymphoma), inflammatory disorders (e.g. inflammatory joint  
 CC disorders and inflammation induced cell damage to the eye, brain and

CC other organs), ischemia or reperfusion injury (e.g. myocardial ischemia  
 CC and reperfusion injury, renal ischemia, spinal cord ischemia and/or  
 CC reperfusion injury, retinal ischemia or infarction, and stroke), toxic  
 CC insult (e.g. liver toxicity, pulmonary toxicity, toxic damage to other  
 CC organs from chemicals, radiation, and other noxious substances), macular  
 CC degeneration, cataract formation, pancreatitis, Crohn's disease,  
 CC ulcerative colitis, accelerated aging, spinal cord disease (e.g. motor  
 CC neuron diseases, degeneration of the spinal cord, Guillan Barre Syndrome  
 CC and demyelinating disease), bypass surgery, chemotherapy, AZT,  
 CC chemically-induced reperfusion, and therapeutics such as clozapine, AZT,  
 CC and anthracyclines.  
 XX  
 SQ Sequence 6 AA;  
 Query Match 100.0%; Score 30; DB 20; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 SVDVEY 6  
 Db 1 SVDVEY 6  
 RESULT 2  
 ABB80001  
 ID ABB80001 standard; peptide; 6 AA.  
 XX  
 AC ABB80001;  
 XX  
 DT 26-JUL-2002 (first entry)  
 XX  
 DE Streptokinase derived peptide#1.  
 XX  
 KW Streptokinase; cell death; apoptosis; necrosis; neurotropic;  
 KW neuroprotective; antiparkinsonian; anticonvulsant; cytostatic;  
 KW antiinflammatory; antiarthritic; antirheumatic; cardiant;  
 KW antiatherosclerotic; vasotropic; immunosuppressive; anti-HIV;  
 KW dermatological; antidiabetic; antianaemic; virucide; ophthalmological;  
 KW antiulcer; antibacterial; antiparasitic; neurodegenerative disease;  
 KW Parkinson's disease; Alzheimer's disease; Huntington's disease;  
 KW cerebellar degeneration; neoplastic disorder; cancer;  
 KW inflammatory disorder; arthritis; inflammatory joint disorders;  
 KW cardiovascular disease; heart failure; atherosclerosis;  
 KW myocardial reperfusion injury; immune disease; autoimmune disease;  
 KW acquired immunodeficiency syndrome; AIDS; rheumatoid arthritis;  
 KW systemic lupus erythematosus; diabetes mellitus; pernicious anaemia;  
 KW myelodegenerative diseases; viral diseases; macular degeneration;  
 KW cataract; Crohn's disease; ulcerative colitis; pancreatitis;  
 KW prion disease; aging.  
 XX  
 OS Synthetic.  
 XX  
 PN US6348567-B1.  
 XX  
 PD 19-FEB-2002.  
 XX  
 PF 19-APR-1999; 99US-0294457.  
 XX  
 PR 06-DEC-1995; 95US-008233P.  
 PR 05-DEC-1996; 96US-0759599.  
 XX  
 (MOLE-) MOLECULAR THERAPEUTICS INC.  
 XX  
 PA Krystal G, Rabkin SW;  
 XX  
 PI WPI; 2002-266542/31.  
 XX  
 DR New peptides obtained from streptokinase, useful in ameliorating cell  
 PT death due to apoptosis and/or necrosis and treating neurodegenerative,  
 PT neoplastic, immune, cardiovascular and inflammatory disorders -  
 XX  
 PS Claim 3; Column 5; 18pp; English.  
 XX

CC The invention relates to an isolated peptide obtained from streptokinase,  
 CC or its derivative or analog, which ameliorate cell death. The activity of  
 CC peptides of the invention may be described as, neurotropic,  
 CC neuroprotective, antiparkinsonian, anticonvulsant, cytostatic,  
 CC antiinflammatory, antiarthritic, antirheumatic, cardiant,  
 CC antiatherosclerotic, vasotropic, immunosuppressive, anti-HIV,  
 CC dermatological, antidiabetic, antianemic, virucide, ophthalmological,  
 CC antiulcer, antibacterial and antiparasitic. Peptides of the invention  
 CC ameliorates apoptosis and necrosis in a warm-blooded animal. Compositions  
 CC comprising peptides of the invention are useful for treating  
 CC neurodegenerative diseases (e.g. Parkinson's, Alzheimer's, Huntington's  
 CC cancer, inflammatory disorders (e.g. arthritis, inflammatory joint  
 CC and myocardial reperfusion injury), immune diseases (e.g. autoimmune  
 CC disease, acquired immunodeficiency syndrome (AIDS), rheumatoid arthritis,  
 CC systemic lupus erythematosus, diabetes mellitus, pernicious anaemia),  
 CC myelodegenerative diseases, viral diseases, and degenerative diseases of  
 CC any organ. Other disorders include macular degeneration, cataracts,  
 CC Crohn's disease, ulcerative colitis, cataracts, pancreatitis, infectious  
 CC diseases including bacteria, parasite, prion-based diseases, and  
 CC accelerated aging. The current sequence represents a streptokinase  
 CC derived peptide of the invention with an ability to ameliorate cell  
 CC death in cardiac myocytes.

XX Sequence 6 AA;

Query Match 100.0%; Score 30; DB 23; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVDFVEY 6  
 |||||  
 Db 1 SVDFVEY 6

# RESULT 3

ID ABB80005 standard; peptide; 16 AA.

AC ABB80005;

DT 26-JUL-2002 (first entry)

XX Streptokinase derived peptide#5.

DE Streptokinase; cell death; apoptosis; necrosis; neurotropic;  
 KW neuroprotective; antiparkinsonian; anticonvulsant; cytostatic;  
 KW antiinflammatory; antiarthritic; antirheumatic; cardiant;  
 KW antiatherosclerotic; vasotropic; immunosuppressive; anti-HIV;  
 KW dermatological; antidiabetic; antianemic; virucide; ophthalmological;  
 KW antiulcer; antibacterial; antiparasitic; neurodegenerative disease;  
 KW Parkinson's disease; Alzheimer's disease; Huntington's disease;  
 KW cerebellar degeneration; neoplastic disorder; cancer;  
 KW inflammatory disorder; arthritis; inflammatory joint disorders;  
 KW cardiovascular disease; heart failure; atherosclerosis;  
 KW myocardial reperfusion injury; immune disease; autoimmune disease;  
 KW acquired immunodeficiency syndrome; AIDS; rheumatoid arthritis;  
 KW systemic lupus erythematosus; diabetes mellitus; pernicious anaemia;  
 KW myelodegenerative diseases; viral diseases; macular degeneration;  
 KW cataract; Crohn's disease; ulcerative colitis; pancreatitis;  
 KW prion disease; aging.

OS Synthetic.

XX US6348567-B1.

XX 19-FEB-2002.

PD 19-APR-1999; 99US-0294457.

PF 06-DEC-1995; 95US-008233P.

PR 05-DEC-1996; 96US-0759599.

XX (MOLE-) MOLECULAR THERAPEUTICS INC.

PA Krystal G, Rabkin SW;

PI WPI; 2002-266542/31.

XX New peptides obtained from streptokinase, useful in ameliorating cell  
 PT death due to apoptosis and/or necrosis and treating neurodegenerative,  
 PT neoplastic, immune, cardiovascular and inflammatory disorders -  
 XX Claim 7; Column 5; 18pp; English.

XX The invention relates to an isolated peptide obtained from streptokinase,  
 CC or its derivative or analog, which ameliorate cell death. The activity of  
 CC peptides of the invention may be described as, neurotropic,  
 CC neuroprotective, antiparkinsonian, anticonvulsant, cytostatic,  
 CC antiinflammatory, antiarthritic, antirheumatic, cardiant,  
 CC antiatherosclerotic, vasotropic, immunosuppressive, anti-HIV,  
 CC dermatological, antidiabetic, antianemic, virucide, ophthalmological,  
 CC antiulcer, antibacterial and antiparasitic. Peptides of the invention  
 CC ameliorates apoptosis and necrosis in a warm-blooded animal. Compositions  
 CC comprising peptides of the invention are useful for treating  
 CC neurodegenerative diseases (e.g. Parkinson's, Alzheimer's, Huntington's  
 CC cancer, inflammatory disorders (e.g. arthritis, inflammatory joint  
 CC disorders), cardiovascular diseases (e.g. heart failure, atherosclerosis  
 CC and myocardial reperfusion injury), immune diseases (e.g. autoimmune  
 CC disease, acquired immunodeficiency syndrome (AIDS), rheumatoid arthritis,  
 CC systemic lupus erythematosus, diabetes mellitus, pernicious anaemia),  
 CC myelodegenerative diseases, viral diseases, and degenerative diseases of  
 CC any organ. Other disorders include macular degeneration, cataracts,  
 CC Crohn's disease, ulcerative colitis, cataracts, pancreatitis, infectious  
 CC diseases including bacteria, parasite, prion-based diseases, and  
 CC accelerated aging. The current sequence represents a streptokinase  
 CC derived peptide of the invention with an ability to ameliorate cell  
 CC death in cardiac myocytes.

XX Sequence 16 AA;

Query Match 100.0%; Score 30; DB 23; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 1.9;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDFVEY 6  
 |||||  
 Db 1 SVDFVEY 6

# RESULT 4

AAAY25013

ID AAY25013 standard; peptide; 18 AA.

AC AAY25013;

XX 23-AUG-1999 (first entry)

DT Streptokinase derived peptide 5 for amelioration of cell death.

DE Streptokinase; cell death; amelioration; treatment; disease; aging; AIDS;  
 KW cellular differentiation; physical insult; trauma; anoxia; hyperthermia;  
 KW hypothermia; brain; spinal cord; kidney; heart; lung; liver; skin; HIV;  
 KW viral disorder; hepatitis; retroviral; infection; encephalitis; AIDS;  
 KW neurodegenerative disorder; Parkinson's disease; Alzheimer's disease;  
 KW Huntington's disease; cerebellar degeneration; cardiovascular disease;  
 KW familial amyotrophic lateral sclerosis; atherosclerosis; heart failure;  
 KW infarction; heart disease; cardiomyopathy; hypertensive; myocardial;  
 KW reperfusion injury; immune disease; rheumatoid arthritis; renal; retinal;  
 KW systemic lupus erythematosus; insulin-dependent; diabetes mellitus;  
 KW pernicious anaemia; dermatomyositis; erythema nodosum; myasthenia gravis;  
 KW Sjogren's syndrome; temporal arthritis; autoimmune polyarthritides;  
 KW Wegener's granulomatosis; glomerulonephritis; anti-phospholipid syndrome;  
 KW neoplastic disorder; leukemia; sarcoma; myeloma; carcinoma; neuroma;

melanoma; cancer; breast; colon; cervix; prostate; Hodgkin's disease;  
 non-Hodgkin's lymphoma; inflammatory disorder; stroke; ischemia;  
 spinal cord; toxic insult; pulmonary; macular degeneration; cataract;  
 pancreatitis, Crohn's disease; ulcerative colitis; motor neuron disease;  
 Guillan Bare Syndrome; demyelinating disease; bypass surgery;  
 chemotherapy; clozapine; AZT; anthracycline.

Synthetic.

US5917013-A.

29-JUN-1999.

05-DEC-1996; 96US-0759599.

06-DEC-1995; 95US-0008233.

05-DEC-1996; 96US-0759599.

(RABK/) RABKIN S W.

Krystal G, Rabkin SW;

WPI; 1999-394231/33.

Peptides that ameliorate cell death useful for treating conditions  
 associated with cellular differentiation

Claim 6; Column 12; 15pp; English.

AA25009-Y25019 are novel peptides derived from streptokinase that  
 ameliorate cell death. The products of the invention and their encoding  
 nucleic acids may be useful for treating diseases and conditions related  
 to aging, cellular differentiation, physical insult (e.g. physical  
 trauma, anoxia, hyperthermia, hypothermia, chemically induced damage,  
 and trauma to the brain, spinal cord, kidney, heart, lungs, liver, skin  
 and any other organ), viral disorders (e.g. hepatitis, retroviral  
 infections, viral encephalitis, and AIDS/HIV), neurodegenerative  
 diseases (e.g. Parkinson's disease, Alzheimer's disease, Huntington's  
 disease, cerebellar degenerations, and familial amyotrophic lateral  
 sclerosis (FALS)), cardiovascular disease (e.g. atherosclerosis,  
 myocardial infarction, heart failure, cardiomyopathy, myocardial  
 reperfusion injury, and hypertensive heart disease), immune disease (e.g.  
 rheumatoid arthritis, systemic lupus erythematosus, insulin-dependent  
 diabetes mellitus, lupus, pernicious anaemia, dermatomyositis, enythem  
 nodosum, Sjogren's syndrome, temporal arthritis, myasthenia gravis,  
 Wegener's granulomatosis, glomerulonephritis, anti-phospholipid syndrome,  
 and autoimmune polyarthritides), a neoplastic disorder (e.g. leukemia,  
 sarcomas, myelomas, carcinomas, neuromas, melanoma, cancers of the  
 breast, brain, colon, cervix, and prostate, Hodgkin's disease and  
 non-Hodgkin's lymphoma), inflammatory disorders (e.g. inflammatory joint  
 disorders and inflammatory induced cell damage to the eye, brain and  
 other organs), ischemia or reperfusion injury (e.g. myocardial ischemia  
 and reperfusion injury, renal ischemia, spinal cord ischemia and/or  
 reperfusion injury, retinal ischemia or infarction, and stroke), toxic  
 insult (e.g. liver toxicity, pulmonary toxicity, toxic damage to other  
 organs from chemicals, radiation, and other noxious substances), macular  
 degeneration, cataract formation, pancreatitis, Crohn's disease, motor  
 ulcerative colitis, accelerated aging, spinal cord disease (e.g. motor  
 neuron diseases, degeneration of the spinal cord, Guillan Bare Syndrome  
 and demyelinating disease), bypass surgery, chemotherapy,  
 chemically-induced reperfusion, and therapeutics such as clozapine, AZT,  
 and anthracyclines.

Sequence 18 AA;

Query Match 100.0%; Score 30; DB 20; Length 18;

Best Local Similarity 100.0%; Pred. No. 2.2;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVDVEY 6

Db 1 SVDVEY 6

RESULT 5

AA25014

ID AA25014 standard; peptide; 20 AA.

XX

AC AA25014;

XX

DT 23-AUG-1999 (first entry)

XX

Streptokinase derived peptide 6 for amelioration of cell death.

XX

Streptokinase; cell death; amelioration; treatment; disease; aging; AIDS;  
 cellular differentiation; physical insult; trauma; anoxia; hyperthermia;  
 hypothermia; brain; spinal cord; kidney; heart; lung; liver; skin; HIV;  
 viral disorder; hepatitis; retroviral; infection; encephalitis; FALS;  
 neurodegenerative disorder; Parkinson's disease; Alzheimer's disease;  
 Huntington's disease; cerebellar degeneration; cardiovascular disease;  
 familial amyotrophic lateral sclerosis; atherosclerosis; heart failure;  
 infarction; heart disease; cardiomyopathy; hypertensive; myocardial;  
 reperfusion injury; immune disease; rheumatoid arthritis; renal; retinal;  
 systemic lupus erythematosus; insulin-dependent; diabetes mellitus;  
 pernicious anaemia; dermatomyositis; enythem nodosum; myasthenia gravis;  
 Sjogren's syndrome; temporal arthritis; autoimmune polyarthritides;  
 Wegener's granulomatosis; glomerulonephritis; anti-phospholipid syndrome;  
 neoplastic disorder; leukemia; sarcoma; melanoma; carcinoma; neuroma;  
 melanoma; cancer; breast; colon; cervix; prostate; Hodgkin's disease;  
 non-Hodgkin's lymphoma; inflammatory disorder; stroke; ischemia;  
 spinal cord; toxic insult; pulmonary; macular degeneration; cataract;  
 pancreatitis, Crohn's disease; ulcerative colitis; motor neuron disease;  
 Guillan Bare Syndrome; demyelinating disease; bypass surgery;  
 chemotherapy; clozapine; AZT; anthracycline.

Synthetic.

US5917013-A.

29-JUN-1999.

05-DEC-1996; 96US-0759599.

06-DEC-1995; 95US-0008233.

05-DEC-1996; 96US-0759599.

(RABK/) RABKIN S W.

Krystal G, Rabkin SW;

WPI; 1999-394231/33.

Peptides that ameliorate cell death useful for treating conditions  
 associated with cellular differentiation

Claim 7; Column 12; 15pp; English.

AA25009-Y25019 are novel peptides derived from streptokinase that  
 ameliorate cell death. The products of the invention and their encoding  
 nucleic acids may be useful for treating diseases and conditions related  
 to aging, cellular differentiation, physical insult (e.g. physical  
 trauma, anoxia, hyperthermia, hypothermia, chemically induced damage,  
 and trauma to the brain, spinal cord, kidney, heart, lungs, liver, skin  
 and any other organ), viral disorders (e.g. hepatitis, retroviral  
 infections, viral encephalitis, and AIDS/HIV), neurodegenerative  
 diseases (e.g. Parkinson's disease, Alzheimer's disease, Huntington's  
 disease, cerebellar degenerations, and familial amyotrophic lateral  
 sclerosis (FALS)), cardiovascular disease (e.g. atherosclerosis,  
 myocardial infarction, heart failure, cardiomyopathy, myocardial  
 reperfusion injury, and hypertensive heart disease), immune disease (e.g.  
 rheumatoid arthritis, systemic lupus erythematosus, insulin-dependent  
 diabetes mellitus, lupus, pernicious anaemia, dermatomyositis, enythem  
 nodosum, Sjogren's syndrome, temporal arthritis, myasthenia gravis,  
 Wegener's granulomatosis, glomerulonephritis, anti-phospholipid syndrome,  
 and autoimmune polyarthritides), a neoplastic disorder (e.g. leukemia,  
 sarcomas, myelomas, carcinomas, neuromas, melanoma, cancers of the

CC breast, brain, colon, cervix, and prostate, Hodgkin's disease and  
CC non-Hodgkin's lymphoma), inflammatory disorders (e.g. inflammatory joint  
CC disorders and inflammation induced cell damage to the eye, brain and  
CC other organs), ischemia or reperfusion injury (e.g. myocardial ischemia  
CC and reperfusion injury, renal ischemia, spinal cord ischemia and/or  
CC reperfusion injury, retinal ischemia or infarction, and stroke), toxic  
CC insult (e.g. liver toxicity, pulmonary toxicity, toxic damage to other  
CC organs from chemicals, radiation, and other noxious substances), macular  
CC degeneration, cataract formation, pancreatitis, Crohn's disease,  
CC ulcerative colitis, accelerated aging, spinal cord disease (e.g. motor  
CC neuron diseases, degeneration of the spinal cord, Guillain Barre Syndrome  
CC and demyelinating disease), bypass surgery, chemotherapy,  
CC and chemically-induced reperfusion, and therapeutics such as clozapine, AZT,  
CC and antrachrycines.  
XX SQ Sequence 20 AA;  
Query Match 100.0%; Score 30; DB 20; Length 20;  
Best Local Similarity 100.0%; Pred. No. 2.4; Indels 0; Gaps 0;  
Matches 6; Conservative 0; Mismatches 0;  
QY 1 SVDVEY 6  
| | | | |  
Db 1 SVDVEY 6  
| | | | |  
RESULT 6  
ABB80006  
ID ABB80006 standard; peptide; 20 AA.  
XX AC ABB80006;  
XX 26-JUL-2002 (first entry)  
DT DT  
DE Streptokinase derived peptide#6.  
XX  
KW Streptokinase; cell death; apoptosis; necrosis; neurotropic;  
KW neuroprotective; antiparkinsonian; anticonvulsant; cytostatic;  
KW anti-inflammatory; antiarthritic; antirheumatic; cardiant;  
KW antiatherosclerotic; vasotropic; immunosuppressive; anti-HIV;  
KW dermatological; antidiabetic; antianaemic; virucide; ophthalmological;  
KW antitumor; antibacterial; antiparasitic; neurodegenerative disease;  
KW Parkinson's disease; Alzheimer's disease; Huntington's disease;  
KW cerebellar degeneration; neoplastic disorder; cancer;  
KW inflammatory disorder; arthritis; inflammatory joint disorders;  
KW cardiovascular disease; heart failure; atherosclerosis;  
KW myocardial reperfusion injury; immune disease; autoimmune disease;  
KW acquired immunodeficiency syndrome; AIDS; rheumatoid arthritis;  
KW systemic lupus erythematosus; diabetes mellitus; pernicious anaemia;  
KW myelodegenerative diseases; viral diseases; macular degeneration;  
KW cataract; Crohn's disease; ulcerative colitis; pancreatitis;  
KW prion disease; aging.  
XX OS Synthetic.  
XX US6348567-B1.  
XX 19-FEB-2002.  
XX 19-APR-1999; 99US-0294457.  
XX 06-DEC-1995; 95US-008233P.  
XX 05-DEC-1996; 96US-0759599.  
XX (MOLE-) MOLECULAR THERAPEUTICS INC.  
XX Krystal G, Rabkin SW;  
XX WPI; 2002-266542/31.  
XX  
XX New peptides obtained from streptokinase, useful in ameliorating cell  
XX death due to apoptosis and/or necrosis and treating neurodegenerative,  
XX neoplastic, immune, cardiovascular and inflammatory disorders -

XX Claim 8; Column 5; 18pp; English.  
XX The invention relates to an isolated peptide obtained from streptokinase,  
XX or its derivative or analog, which ameliorate cell death. The activity of  
XX peptides of the invention may be described as, neurotropic,  
XX neuroprotective, antiparkinsonian, anticonvulsant, cytostatic,  
XX anti-inflammatory, antiarthritic, antirheumatic, cardiant,  
XX antiatherosclerotic, vasotropic, immunosuppressive, anti-HIV,  
XX dermatological, antidiabetic, antianaemic, virucide, ophthalmological,  
XX antitumor, antibacterial and antiparasitic. Peptides of the invention  
XX ameliorates apoptosis and necrosis in a warm-blooded animal. Compositions  
XX comprising peptides of the invention are useful for treating  
XX neurodegenerative diseases (e.g. Parkinson's, Alzheimer's, Huntington's  
XX disease and cerebellar degeneration) neoplastic disorders including  
XX cancer, inflammatory disorders (e.g. arthritis, inflammatory joint  
XX disorders), cardiovascular diseases (e.g. heart failure, atherosclerosis  
XX and myocardial reperfusion injury), immune diseases (e.g. autoimmune  
XX disease, acquired immunodeficiency syndrome (AIDS), rheumatoid arthritis,  
XX systemic lupus erythematosus, diabetes mellitus, pernicious anaemia),  
XX myelodegenerative diseases, viral diseases, and degenerative diseases of  
XX any organ. Other disorders include macular degeneration, cataracts,  
XX Crohn's disease, ulcerative colitis, cataracts, pancreatitis, infectious  
XX diseases including bacteria, parasite, prion-based diseases, and  
XX accelerated aging. The current sequence represents a streptokinase  
XX derived peptide of the invention with an ability to ameliorate cell  
XX death in cardiac myocytes.  
XX SQ Sequence 20 AA;  
Query Match 100.0%; Score 30; DB 23; Length 20;  
Best Local Similarity 100.0%; Pred. No. 2.4; Indels 0; Gaps 0;  
Matches 6; Conservative 0; Mismatches 0;  
QY 1 SVDVEY 6  
| | | | |  
Db 1 SVDVEY 6  
| | | | |  
RESULT 7  
ABG76052  
ID ABG76052 standard; peptide; 20 AA.  
XX AC ABG76052;  
XX 20-MAY-2003 (first entry)  
DT DT  
DE Streptokinase fragment based, cell death ameliorating, 20mer peptide.  
XX  
KW Cell death; streptokinase; neurodegenerative disorder; leukaemia; AIDS;  
KW Parkinson's disease; Alzheimer's disease; cardiovascular disease; trauma;  
KW atherosclerosis; myocardial infarction; immune disease; carcinoma;  
KW rheumatoid arthritis; neoplastic disorder; inflammatory disorder;  
KW arthritis; inflammatory induced cell damage; motor neuron disease;  
KW physical insult; severe shock; ischaemia; reperfusion injury; hepatitis;  
KW cell death associated procedure; spinal cord reperfusion injury;  
KW toxic insult; liver toxicity; pulmonary toxicity; spinal cord disease;  
KW Guillain-Barre syndrome; bypass surgery; myocardial ischaemia;  
KW chemotherapy; viral disease; viral encephalitis; infectious disease;  
KW bacterial disease; prion-based disease; macular degeneration;  
KW cataract formation; pancreatitis; Crohn's disease; ulcerative colitis;  
KW accelerated aging; oxidative stress.  
XX OS Synthetic.  
XX US2002165129-A1.  
XX 07-NOV-2002.  
XX 31-JUL-2001; 2001US-0919703.  
XX 06-DEC-1995; 95US-008233P.  
XX 19-APR-1999; 99US-0294457.

PR 05-DEC-1996; 96US-0759599.  
 XX (KRYSTAL G. RABKIN S. W.)  
 PA (RABKIN S. W.)  
 XX Krystal G. Rabkin SW;  
 XX WPI; 2003-246673/25.  
 DR  
 XX  
 XX Pharmaceutical composition for treating e.g. neurodegenerative  
 PT disorder, cardiovascular disease, neoplastic disorder, viral disease  
 PT and immune diseases, comprises a peptide capable of ameliorating cell  
 PT death  
 XX  
 XX  
 XX Claim 2; Page 3; 19pp; English.  
 PS  
 XX  
 CC The invention relates to a pharmaceutical composition, which comprises a  
 CC peptide capable of ameliorating cell death, its derivative or analogue,  
 CC comprising a sequence Val-Asp-Val, where the peptide is in a suitable  
 CC pharmaceutical carrier or diluent. The pharmaceutical composition  
 CC (comprising the peptide) is useful for treating or preventing cell  
 CC death associated with a neurodegenerative disorder e.g. Parkinson's  
 CC disease and Alzheimer's disease; cardiovascular disease e.g.  
 CC atherosclerosis and myocardial infarction; immune disease e.g. AIDS and  
 CC rheumatoid arthritis; neoplastic disorders e.g. leukaemia and carcinoma;  
 CC inflammatory disorder e.g. arthritis and inflammatory induced cell  
 CC damage; disease caused by physical insult e.g. trauma and severe shock;  
 CC ischaemia or reperfusion injury e.g. myocardial ischaemia and spinal cord  
 CC reperfusion injury; toxic insult e.g. liver toxicity and pulmonary  
 CC toxicity; spinal cord disease e.g. motor neuron disease and Guillain-Barre  
 CC syndrome; procedures associated with cell death e.g. bypass surgery and  
 CC chemotherapy; viral disease e.g. hepatitis and viral encephalitis;  
 CC infectious diseases e.g. bacterial disease and prion-based disease;  
 CC macular degeneration; cataract formation; pancreatitis; Crohn's disease;  
 CC ulcerative colitis; accelerated aging and oxidative stress in a warm-  
 CC blooded animal. The present sequence represents the amino acid sequence  
 CC of a 20mer peptide capable of ameliorating cell death which is based on a  
 CC streptokinase fragment.  
 XX  
 XX Sequence 20 AA;  
 SQ  
 Query Match 100.0%; Score 30; DB 24; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 2.4;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SVDVEY 6  
 DB 1 SVDVEY 6  
 RESULT 8  
 ID AAY25015 standard; peptide; 21 AA.  
 XX  
 AC AAY25015;  
 XX  
 DT 23-AUG-1999 (first entry)  
 XX  
 DE Streptokinase derived peptide 7 for amelioration of cell death.  
 XX  
 KW Streptokinase; cell death; amelioration; treatment; disease; aging; AIDS;  
 KW cellular differentiation; physical insult; trauma; anoxia; hyperthermia;  
 KW hypothermia; brain; spinal cord; kidney; heart; lung; liver; skin; HIV;  
 KW viral disorder; hepatitis; retroviral; infection; encephalitis; AIDS;  
 KW neurodegenerative disorder; Parkinson's disease; Alzheimer's disease;  
 KW Huntington's disease; cerebellar degeneration; cardiovascular disease;  
 KW familial amyotrophic lateral sclerosis; atherosclerosis; heart failure;  
 KW infarction; heart disease; cardiomyopathy; hypertensive; myocardial;  
 KW reperfusion injury; immune disease; rheumatoid arthritis; renal; retinal;  
 KW systemic lupus erythematosus; insulin-dependent; diabetes mellitus;  
 KW pernicious anaemia; dermatomyositis; enythemia nodosum; myasthenia gravis;  
 KW Sjogren's syndrome; temporal arthritis; autoimmune polyarthritides;  
 KW Wegener's granulomatosis; glomerulonephritis; anti-phospholipid syndrome;

KW neoplastic disorder; leukemia; sarcoma; myeloma; carcinoma; neuroma;  
 KW melanoma; cancer; breast; colon; cervix; prostate; Hodgkin's disease;  
 KW non-Hodgkin's lymphoma; inflammatory disorder; stroke; ischemia;  
 KW spinal cord; toxic insult; pulmonary; macular degeneration; cataract;  
 KW pancreatitis; Crohn's disease; ulcerative colitis; motor neuron disease;  
 KW Guillan Bare Syndrome; demyelinating disease; bypass surgery;  
 KW chemotherapy; clozapine; AZT; anthracycline.  
 XX  
 OS Synthetic.  
 XX  
 XX US5917013-A.  
 PN  
 XX  
 PD 29-JUN-1999.  
 XX  
 XX  
 PF 05-DEC-1996; 96US-0759599.  
 XX  
 PR 06-DEC-1995; 95US-0008233.  
 PR 05-DEC-1996; 96US-0759599.  
 XX  
 PA (RABKIN S. W.)  
 XX  
 XX Krystal G. Rabkin SW;  
 PI WPI; 1999-394231/33.  
 XX  
 DR Peptides that ameliorate cell death useful for treating conditions  
 XX associated with cellular differentiation  
 PT  
 PT  
 XX  
 PS Claim 9; Column 12; 15pp; English.  
 XX  
 CC AAY25009-Y25019 are novel peptides derived from streptokinase that  
 CC ameliorate cell death. The products of the invention and their encoding  
 CC nucleic acids may be useful for treating diseases and conditions related  
 CC to aging, cellular differentiation, physical insult (e.g. physical  
 CC trauma, anoxia, hyperthermia, hypothermia, chemically induced damage,  
 CC and trauma to the brain, spinal cord, kidney, heart, lungs, liver, skin  
 CC and any other organ), viral disorders (e.g. hepatitis, retroviral  
 CC infections, viral encephalitis, and AIDS/HIV), neurodegenerative  
 CC disorders (e.g. Parkinson's disease, Alzheimer's disease, Huntington's  
 CC disease, cerebellar degenerations, and familial amyotrophic lateral  
 CC sclerosis (FALS)), cardiovascular disease (e.g. atherosclerosis,  
 CC myocardial infarction, heart failure, cardiomyopathy, myocardial  
 CC reperfusion injury, and hypertensive heart disease), immune disease (e.g.  
 CC rheumatoid arthritis, systemic lupus erythematosus, insulin-dependent,  
 CC diabetes mellitus, lupus, pernicious anaemia, dermatomyositis, enythemia  
 CC nodosum, Sjogren's syndrome, temporal arthritis, myasthenia gravis,  
 CC Wegener's granulomatosis, glomerulonephritis, anti-phospholipid syndrome,  
 CC and autoimmune polyarthritides), a neoplastic disorder (e.g. leukemia,  
 CC sarcomas, myelomas, carcinomas, neuromas, melanoma, cancers of the  
 CC breast, brain, colon, cervix, and prostate, Hodgkin's disease and  
 CC non-Hodgkin's lymphoma), inflammatory disorders (e.g. inflammatory joint  
 CC disorders and inflammatory induced cell damage to the eye, brain and  
 CC other organs), ischemia or reperfusion injury (e.g. myocardial ischemia  
 CC and reperfusion injury, renal ischemia, spinal cord ischemia and/or  
 CC insult (e.g. liver toxicity, pulmonary toxicity, toxic damage to other  
 CC organs from chemicals, radiation, and other noxious substances), macular  
 CC degeneration, cataract formation, pancreatitis, Crohn's disease,  
 CC ulcerative colitis, accelerated aging, spinal cord disease (e.g. motor  
 CC neuron diseases, degeneration of the spinal cord, Guillan Bare Syndrome  
 CC and demyelinating disease), bypass surgery, chemotherapy,  
 CC chemically-induced reperfusion, and therapeutics such as clozapine, AZT,  
 CC and anthracyclines.  
 XX  
 SQ Sequence 21 AA;  
 Query Match 100.0%; Score 30; DB 20; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 2.6;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SVDVEY 6  
 DB 1 SVDVEY 6

RESULT 9  
ABB80007  
ID ABB80007 standard; peptide; 21 AA.  
XX  
AC ABB80007;  
XX  
DT 26-JUL-2002 (first entry)  
XX  
DE Streptokinase derived peptide#7.  
XX  
XX Streptokinase; cell death; apoptosis; necrosis; neuroprotection; neuroprotective; antiparkinsonian; anticonvulsant; cytostatic;  
KW antiinflammatory; antiarthritic; antirheumatic; cardiant;  
KW antiatherosclerotic; vasotropic; immunosuppressive; anti-HIV;  
KW dermatological; antidiabetic; antianaemic; virucide; ophthalmological;  
KW antitumor; antibacterial; antiparasitic; neurodegenerative disease;  
KW Parkinson's disease; Alzheimer's disease; Huntington's disease;  
KW cerebellar degeneration; neoplastic disorder; cancer;  
KW inflammatory disorder; arthritis; inflammatory joint disorders;  
KW cardiovascular disease; heart failure; atherosclerosis;  
KW myocardial reperfusion injury; immune disease; autoimmune disease;  
KW acquired immunodeficiency syndrome; AIDS; rheumatoid arthritis;  
KW systemic lupus erythematosus; diabetes mellitus; pernicious anaemia;  
KW myelodegenerative diseases; viral diseases; macular degeneration;  
KW cataract; Crohn's disease; ulcerative colitis; pancreatitis;  
KW prion disease; aging.  
XX  
OS Synthetic.  
XX  
XX US6348567-B1.  
PN  
XX  
PD 19-FEB-2002.  
XX  
XX 19-APR-1999; 99US-0294457.  
PF  
XX  
XX 06-DEC-1995; 95US-008233P.  
PR  
XX  
XX 05-DEC-1996; 96US-0759599.  
PR  
XX  
PA (MOLE-) MOLECULAR THERAPEUTICS INC.  
XX  
XX Krystal G, Rabkin SW;  
PI  
XX  
XX WPI; 2002-266542/31.  
DR  
XX  
XX New peptides obtained from streptokinase, useful in ameliorating cell  
PT death due to apoptosis and/or necrosis and treating neurodegenerative,  
PT neoplastic, immune, cardiovascular and inflammatory disorders -  
XX  
XX Claim 9; Column 5; 18pp; English.  
XX  
XX The invention relates to an isolated peptide obtained from streptokinase,  
CC or its derivative or analog, which ameliorate cell death. The activity of  
CC peptides of the invention may be described as, neuroprotection,  
CC neuroprotective, antiparkinsonian, anticonvulsant, cytostatic,  
CC antiinflammatory, antiarthritic, antirheumatic, cardiant,  
CC antiatherosclerotic, vasotropic, immunosuppressive, anti-HIV,  
CC dermatological, antidiabetic, antianaemic, virucide, ophthalmological,  
CC antitumor, antibacterial and antiparasitic. Peptides of the invention  
CC ameliorates apoptosis and necrosis in a warm-blooded animal. Compositions  
CC comprising peptides of the invention are useful for treating  
CC neurodegenerative diseases (e.g. Parkinson's, Alzheimer's, Huntington's  
CC disease and cerebellar degeneration) neoplastic disorders including  
CC cancer, inflammatory disorders (e.g. arthritis, inflammatory joint  
CC disorders), cardiovascular diseases (e.g. heart failure, atherosclerosis  
CC and myocardial reperfusion injury), immune diseases (e.g. autoimmune  
CC disease, acquired immunodeficiency syndrome (AIDS), rheumatoid arthritis,  
CC systemic lupus erythematosus, diabetes mellitus, pernicious anaemia),  
CC myelodegenerative diseases, viral diseases, and degenerative diseases of  
CC any organ. Other disorders include macular degeneration, cataracts,  
CC Crohn's disease, ulcerative colitis, cataracts, pancreatitis, infectious  
CC diseases including bacteria, parasite, prion-based diseases, and

CC accelerated aging. The current sequence represents a streptokinase  
CC derived peptide of the invention with an ability to ameliorate cell  
CC death in cardiac myocytes.  
XX  
SQ Sequence 21 AA;  
Query Match 100.0%; Score 30; DB 23; Length 21;  
Best Local Similarity 100.0%; Pred. No. 2.6;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SVDVEY 6  
Db 1 SVDVEY 6  
RESULT 10  
AA01550  
ID AA01550 standard; peptide; 71 AA.  
XX  
AC AA01550;  
XX  
DT 18-JUN-1999 (first entry)  
XX  
DE Antigenic epitope of streptokinase, spanning amino acids 138-208.  
XX  
KW Antigenic peptide; streptokinase; streptokinase-specific antibody;  
KW thrombolytic activity; thrombolytic therapy; glomerulonephritis;  
KW rheumatic fever.  
XX  
OS Streptococcus equisimilis.  
XX  
XX WO9908698-A1.  
PN  
XX  
PD 25-FEB-1999.  
XX  
XX 18-AUG-1998; 98WO-US17114.  
PF  
XX  
XX 18-AUG-1997; 97US-0055911.  
PR  
XX  
XX (GEO) GEN HOSPITAL CORP.  
PA (HARD) HARVARD COLLEGE.  
XX  
XX Parhami-Seren B, Reed GL;  
PI  
XX  
XX WPI; 1999-190113/16.  
DR  
XX  
XX New polypeptides which bind streptokinase-specific antibodies -  
PT useful in thrombolytic therapy  
PT  
XX  
XX Claim 16; Page 5; 44pp; English.  
XX  
XX The present sequence represents an antigenic epitope of  
CC streptokinase. The specification describes a polypeptide  
CC which binds to a streptokinase-specific antibody and prevents the  
CC antibody binding to native streptokinase. The specification also  
CC describes a synthetic polypeptide (P1) comprising an epitope which  
CC binds to a streptokinase-specific antibody and reduces thrombolytic  
CC activity of streptokinase. P1 is used in thrombolytic therapy, and to  
CC prevent or treat glomerulonephritis and rheumatic fever.  
XX  
SQ Sequence 71 AA;  
Query Match 100.0%; Score 30; DB 20; Length 71;  
Best Local Similarity 100.0%; Pred. No. 10;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SVDVEY 6  
Db 20 SVDVEY 25  
RESULT 11  
AA01558



ID AAY01558 standard; peptide; 146 AA.  
 XX AAY01558;  
 AC  
 XX  
 XX  
 DT 18-JUN-1999 (first entry)  
 XX  
 DE Peptide corresponding to amino acids 148-293 of streptokinase.  
 XX  
 XX Antigenic peptide; streptokinase; streptokinase-specific antibody;  
 KW thrombolytic activity; thrombolytic therapy; glomerulonephritis;  
 KW rheumatic fever.  
 XX  
 OS Streptococcus equisimilis.  
 XX  
 XX WO9908698-A1.  
 PN  
 XX  
 XX 25-FEB-1999.  
 PD  
 XX 18-AUG-1998; 98WO-US17114.  
 PF  
 XX 18-AUG-1997; 97US-0055911.  
 PR  
 XX (GEHO ) GEN HOSPITAL CORP.  
 PA (HARD ) HARVARD COLLEGE.  
 PA  
 XX Parhami-Seren B, Reed GL;  
 XX  
 XX WPI; 1999-190113/16.  
 DR  
 XX  
 XX New polypeptides which bind streptokinase-specific antibodies -  
 FT useful in thrombolytic therapy  
 PT  
 XX Disclosure; Page 13; 44pp; English.  
 PS  
 XX  
 XX The present sequence represents a peptide corresponding to  
 CC amino acids 148-293 of streptokinase. The specification describes a  
 CC polypeptide which binds to a streptokinase-specific antibody and  
 CC prevents the antibody binding to native streptokinase. The specification  
 CC also describes a synthetic polypeptide (PI) comprising an epitope which  
 CC binds to an streptokinase-specific antibody and reduces thrombolytic  
 CC activity of streptokinase. PI is used in thrombolytic therapy, and to  
 CC prevent or treat glomerulonephritis and rheumatic fever.  
 CC  
 XX  
 SQ Sequence 146 AA;  
 Query Match 100.0%; Score 30; DB 20; Length 146;  
 Best Local Similarity 100.0%; Pred. No. 23;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SVDVEY 6  
 DB 10 SVDVEY 15  
 |||||  
 |||||  
 RESULT 12  
 AAY24796  
 ID AAY24796 standard; Protein; 150 AA.  
 XX  
 AC AAY24796;  
 XX  
 XX  
 DT 26-AUG-1999 (first entry)  
 XX  
 DE Recombinant streptokinase RSK144-293.  
 XX  
 KW Streptococcus; streptokinase; fibrin-dependent plasminogen activator;  
 XX nSK; RSK; bacterial; blood clot; thrombotic condition;  
 KW myocardial infarction; venous thrombosis; pulmonary embolism;  
 KW cerebral thrombosis; graft thrombosis; arterial thrombosis.  
 XX  
 OS Streptococcus equisimilis.  
 XX Synthetic.  
 OS  
 XX WO991247-A1.  
 PN

XX 24-JUN-1999.  
 PD  
 XX 15-DEC-1998; 98WO-US26694.  
 PF  
 XX 15-DEC-1997; 97US-0069497.  
 PR  
 XX (HARD ) HARVARD COLLEGE.  
 PA  
 XX Reed GL;  
 PI  
 XX WPI; 1999-395183/33.  
 DR N-PSDB; AAX80494.  
 DR  
 XX N-terminally deleted streptokinase  
 PT  
 XX  
 PS Claim 34; Page 67-68; 73pp; English.  
 XX  
 CC The present invention describes an isolated bacterial protein that  
 CC induces fibrin-dependent plasminogen activation in a pharmaceutical  
 CC composition for dissolving blood clots. Also described are: (1) a  
 CC composition comprising an isolated modified streptokinase, the  
 CC modification being removal of amino acid residues in the amino terminus;  
 CC (2) a method for dissolving a blood clot in a subject, comprising  
 CC administering to the subject a fibrin-dependent streptokinase protein;  
 CC a nucleic acid (1) encoding a modified bacterial streptokinase; (3) an  
 CC expression vector comprising (1); and (4) a host cell transformed with  
 CC the expression vector of (3). The pharmaceutical composition comprising  
 CC a bacterial fibrin-dependent plasminogen activator is useful for  
 CC dissolving blood clots in patients with a thrombotic condition, e.g.  
 CC myocardial infarction, venous thrombosis, pulmonary embolism, cerebral  
 CC thrombosis, graft thrombosis and arterial thrombosis. The modified  
 CC streptokinase can also be used in non-human mammals. Streptokinase  
 CC activation of plasminogen is at least 10-fold, preferably 100-fold  
 CC greater in the presence of fibrin than in the absence of fibrin. The  
 CC modified streptokinase has at least one amino acid substitution that  
 CC inactivates a substrate site for proteolytic cleavage. This reduces the  
 CC rate of degradation of the streptokinase at least two-fold. The present  
 CC sequence represents recombinant streptokinase, designated RSK144-293.  
 XX  
 SQ Sequence 150 AA;  
 Query Match 100.0%; Score 30; DB 20; Length 150;  
 Best Local Similarity 100.0%; Pred. No. 24;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SVDVEY 6  
 DB 14 SVDVEY 19  
 |||||  
 |||||  
 RESULT 13  
 AAY01557  
 ID AAY01557 standard; peptide; 233 AA.  
 XX  
 AC AAY01557;  
 XX  
 XX 18-JUN-1999 (first entry)  
 DT  
 XX  
 DE Peptide corresponding to amino acids 120-352 of streptokinase.  
 XX  
 KW Antigenic peptide; streptokinase; streptokinase-specific antibody;  
 KW thrombolytic activity; thrombolytic therapy; glomerulonephritis;  
 KW rheumatic fever.  
 XX  
 OS Streptococcus equisimilis.  
 XX  
 XX WO9908698-A1.  
 PN  
 XX 25-FEB-1999.  
 PD  
 XX 18-AUG-1998; 98WO-US17114.  
 PF  
 XX



PR 18-AUG-1997; 97US-0055911.  
XX  
PA (GEHO ) GEN HOSPITAL CORP.  
PA (HARD ) HARVARD COLLEGE.  
XX  
PI Parhami-Seren B, Reed GL;  
XX  
XX WPI; 1999-190113/16.  
DR  
XX  
PT New polypeptides which bind streptokinase-specific antibodies -  
PT useful in thrombolytic therapy  
XX  
PS Disclosure; Page 13; 44pp; English.  
XX  
XX The present sequence represents a peptide corresponding to  
CC amino acids 120-352 of streptokinase. The specification describes a  
CC polypeptide which binds to a streptokinase-specific antibody and  
CC prevents the antibody binding to native streptokinase. The specification  
CC also describes a synthetic polypeptide (PI) comprising an epitope which  
CC binds to a streptokinase-specific antibody and reduces thrombolytic  
CC activity of streptokinase. PI is used in thrombolytic therapy, and to  
CC prevent or treat glomerulonephritis and rheumatic fever.  
XX  
SQ Sequence 233 AA;

Query Match 100.0%; Score 30; DB 20; Length 233;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 1 SVDVEY 6  
Db 38 SVDVEY 43  
|||||

RESULT 14  
AAR91599  
ID AAR91599 standard; Protein; 297 AA.\*  
XX  
AC AAR91599;  
XX  
XX 08-AUG-1996 (first entry)  
XX  
XX Streptokinase from pST-1.  
DE  
XX streptokinase; recombinant production; haemolytic Streptococcus.  
KW Synthetic.  
OS  
XX WO9527050-A1.  
EN  
XX 12-OCT-1995.  
PD  
XX 03-APR-1995; 95WO-CN00024.  
PF  
XX 04-APR-1994; 94CN-0112106.  
PR  
XX (UYSH-) UNIV SHANGHAI MEDICAL.  
PA  
XX Song H;  
PI  
XX WPI; 1995-358628/46.  
DR N-PSDB; AAT29961.  
XX  
XX Prepn. of streptokinase - useful for treating thrombus diseases.  
PT  
XX Example 2; Page 6-8; 24pp; Chinese.

The present sequence is that of streptokinase encoded by a pST-1 HindIII fragment. Recombinant streptokinase can be produced by culturing bacteria transformed with a high efficiency plasmid contg. the streptokinase gene, amplified by using haemolytic Streptococcus as the template and using inducers based on the streptokinase nucleotide sequence. The recombinant streptokinase is used to treat thrombotic

DT 26-AUG-1999 (first entry)  
 XX Recombinant streptokinase RSK59-414.  
 DE Streptococcus; streptokinase; fibrin-dependent plasminogen activator;  
 XX nSK; RSK; bacterial; blood clot; thrombotic condition;  
 KW myocardial infarction; venous thrombosis; pulmonary embolism;  
 KW cerebral thrombosis; graft thrombosis; arterial thrombosis.  
 XX Streptococcus equisimilis.  
 OS Synthetic.  
 XX WO9931247-A1.  
 XX 24-JUN-1999.  
 XX 15-DEC-1998; 98WO-US26594.  
 XX 15-DEC-1997; 97US-0069497.  
 XX (HARD ) HARVARD COLLEGE.  
 XX Reed GL;  
 XX WPI; 1999-395183/33.  
 DR N-PSDB; AAX80493.  
 XX N-terminally deleted streptokinase  
 PT Claim 35; Page 65-66; 73pp; English.  
 XX The present invention describes an isolated bacterial protein that  
 CC induces fibrin-dependent plasminogen activation in a pharmaceutical  
 CC composition for dissolving blood clots. Also described are: (1) a  
 CC composition comprising an isolated modified streptokinase, the  
 CC modification being removal of amino acid residues in the amino terminus;  
 CC (2) a method for dissolving a blood clot in a subject, comprising  
 CC administering to the subject a fibrin-dependent streptokinase protein;  
 CC a nucleic acid (I) encoding a modified bacterial streptokinase; (3) an  
 CC expression vector comprising (1); and (4) a host cell transformed with  
 CC the expression vector of (3). The pharmaceutical composition comprising  
 CC a bacterial fibrin-dependent plasminogen activator is useful for  
 CC dissolving blood clots in patients with a thrombotic condition, e.g.  
 CC myocardial infarction, venous thrombosis, pulmonary embolism, cerebral  
 CC thrombosis, graft thrombosis and arterial thrombosis. The modified  
 CC streptokinase can also be used in non-human mammals. Streptokinase  
 CC activation of plasminogen is at least 10-fold, preferably 100-fold  
 CC greater in the presence of fibrin than in the absence of fibrin. The  
 CC modified streptokinase has at least one amino acid substitution that  
 CC inactivates a substrate site for proteolytic cleavage. This reduces the  
 CC rate of degradation of the streptokinase at least two-fold. The present  
 CC sequence represents recombinant streptokinase, designated RSK59-414.  
 XX  
 SQ Sequence 356 AA;  
 Query Match 100.0%; Score 30; DB 20; Length 356;  
 Best Local Similarity 100.0%; Pred. No. 64;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SVDVEY 6  
 DB 99 SVDVEY 104  
 RESULT 17  
 AAR12892  
 ID AAR12892 standard; Protein; 369 AA.  
 XX AAR12892;  
 AC AAR12892;  
 XX 25-MAR-2003 (updated)  
 DT 17-SEP-1991 (first entry)  
 XX

DE Truncated Met streptokinase.  
 XX Fusion protein; blood clotting; coagulation; fibrinolysis;  
 KW antithrombotic; thrombolysis; streptokinase; thrombin.  
 XX Streptococcus equisimilis ATCC 9542 or ATCC 10009.  
 OS  
 FH Key Location/Qualifiers  
 FT Protein 2..369  
 FT /label= core streptokinase  
 FT /note= "AAs 16-383"  
 XX WO9109125-A.  
 XX 27-JUN-1991.  
 XX 07-DEC-1990; 90WO-GB01911.  
 XX 07-DEC-1990; 90WO-GB01911.  
 PR 07-DEC-1989; 89GB-0027722.  
 XX (BRBI-) BRITISH BIO-TECHNOLOGY LTD.  
 XX Dawson KM, Hunter MG, Czaplewski LG;  
 PI WPI; 1991-208151/28.  
 DR N-PSDB; AAQ12159.  
 DR Fusion protein cleavage by blood clotting enzyme - for prodn. of  
 PT fractions having greater antithrombotic activity for therapy and  
 PT prophylaxis.  
 XX Disclosure; Page 88; 115pp; English.  
 XX The sequence was deduced from DNA obtd. from PCR amplified chromo-  
 CC somal DNA from S. equisimilis (Lancefield's Gp C ) ATCC 10009 or  
 CC ATCC 9642. The gene was truncated by 15 codons at the 3' ter-  
 CC minal and engineered to add a Met codon prior to codon 16 of the  
 CC streptokinase CDS. The construct was used to prepare expression  
 CC vector pGC606 for prodn. of the streptokinase core molecule.  
 CC See also AAR12887-R12889, AAR12891-R12893, AAR12885 and AAR12522.  
 CC (Updated on 25-MAR-2003 to correct PA field.)  
 XX SQ Sequence 369 AA;  
 Query Match 100.0%; Score 30; DB 12; Length 369;  
 Best Local Similarity 100.0%; Pred. No. 67;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SVDVEY 6  
 DB 143 SVDVEY 148  
 RESULT 18  
 AAR10195  
 ID AAR10195 standard; Protein; 371 AA.  
 XX AAR10195;  
 AC AAR10195;  
 XX 28-MAR-1991 (first entry)  
 DT Streptokinase (1-372, Phe 118 deleted).  
 DE streptokinase; thrombolytic agent; myocardial infarction.  
 XX Synthetic.  
 XX EP407942-A.  
 XX 16-JAN-1991.  
 PD 09-JUL-1990; 90EP-0113099.  
 PF

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XX 11-APR-1990; 90JP-0096830.
PR 11-JUL-1989; 89JP-0179432.
PR 27-NOV-1989; 89JP-0307957.
XX (SAKA ) OTSUKA PHARM FACTOR.
XX
XX Majima E, Ogino K, Ono K, Sakata Y, Uenoyama T;
XX WPI; 1991-016179/03.
XX
XX Synthetic gene encoding streptokinase - scale, high purity prodn.
PT of streptokinase used as a thrombolytic agent
XX
XX Claim 8; Page 59; 76pp; English.
XX
XX Streptokinase derivative having a C-terminal deletion (i.e. Pro
CC 373-Lys 414) and Phe at position 118 being deleted. Alternatively,
CC Phe 118 can be replaced with any other amino acid. Derivatives show
CC a decreased antigenicity, higher stability in blood and greater
CC selectivity of thrombolytic activity and specificity.
CC The protein is used as a thrombolytic agent in
CC patients with lung thrombus or myocardial infarction.
CC See also AAQ10230 and AAR10196-R10200.
XX
XX Sequence 371 AA;
Query Match 100.0%; Score 30; DB 12; Length 371;
Best Local Similarity 100.0%; Pred. No. 67;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SVDVEY 6
DB 156 SVDVEY 161
|||||
RESULT 19
AAR10197
ID AAR10197 standard; Protein; 372 AA.
XX
XX AAR10197;
XX
XX 28-MAR-1991 (first entry)
XX
XX Streptokinase (1-372, Gln 256, Gln 257).
XX
XX streptokinase; thrombolytic agent; myocardial infarction.
XX
XX Synthetic.
XX
XX EP407942-A.
XX
XX 16-JAN-1991.
XX
XX 09-JUL-1990; 90EP-0113099.
XX
XX 11-APR-1990; 90JP-0096830.
PR 11-JUL-1989; 89JP-0179432.
PR 27-NOV-1989; 89JP-0307957.
XX
XX (SAKA ) OTSUKA PHARM FACTOR.
XX
XX Majima E, Ogino K, Ono K, Sakata Y, Uenoyama T;
XX WPI; 1991-016179/03.
XX
XX Synthetic gene encoding streptokinase - scale, high purity prodn.
PT of streptokinase used as a thrombolytic agent
XX
XX Claim 9; Page 59; 76pp; English.
XX
XX Streptokinase derivative having a C-terminal deletion (i.e. Pro
CC 373-Lys 414) and Gln being substituted for Lys at both positions

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CC 256 and 257. Derivatives show a decreased antigenicity, higher
CC stability in blood and greater selectivity of thrombolytic activity
CC and specificity. The protein is used as a thrombolytic agent in
CC patients with lung thrombus or myocardial infarction.
CC See also AAQ10230, AAR10195-6 and AAR10198-R10200.
XX
XX Sequence 372 AA;
Query Match 100.0%; Score 30; DB 12; Length 372;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SVDVEY 6
DB 157 SVDVEY 162
|||||
RESULT 20
AAR10200
ID AAR10200 standard; Protein; 372 AA.
XX
XX AAR10200;
XX
XX 28-MAR-1991 (first entry)
XX
XX Streptokinase (1-372) derivative.
XX
XX streptokinase; thrombolytic agent; myocardial infarction.
XX
XX Synthetic.
XX
XX EP407942-A.
XX
XX 16-JAN-1991.
XX
XX 09-JUL-1990; 90EP-0113099.
XX
XX 11-APR-1990; 90JP-0096830.
PR 11-JUL-1989; 89JP-0179432.
PR 27-NOV-1989; 89JP-0307957.
XX
XX (SAKA ) OTSUKA PHARM FACTOR.
XX
XX Majima E, Ogino K, Ono K, Sakata Y, Uenoyama T;
XX WPI; 1991-016179/03.
XX
XX Synthetic gene encoding streptokinase - scale, high purity prodn.
PT of streptokinase used as a thrombolytic agent
XX
XX Claim 6; Page 59; 76pp; English.
XX
XX Streptokinase derivative having a C-terminal deletion (i.e. Pro
CC 373-Lys 414) and retaining streptokinase activity. One or more of
CC the amino acids can be replaced by a different amino acid at the
CC same position or it can be deleted. Alternatively, an extra residue
CC can be inserted into the sequence. Derivatives show
CC a decreased antigenicity, higher stability in blood and greater
CC selectivity of thrombolytic activity and specificity.
CC The protein is used as a thrombolytic agent in
CC patients with lung thrombus or myocardial infarction.
CC See also AAQ10230 and AAR10195-R10199.
XX
XX Sequence 372 AA;
Query Match 100.0%; Score 30; DB 12; Length 372;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SVDVEY 6
DB 157 SVDVEY 162
|||||

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RESULT 21
AA84006
ID  AA84006 standard; Protein; 372 AA.
XX
XX  AA84006;
XX  AC
XX  DT 03-JUL-2000 (first entry)
XX  DE
XX  DE Amino acid sequence of a mutant streptokinase.
XX
XX  Streptokinase; SKC-2; plasminogen; plasmin; antigenicity;
XX  plasminogen activator complex formation; thrombolytic;
XX  myocardial infarction; pulmonary thromboembolism; thrombosis.
XX
XX  Synthetic.
XX  OS Streptococcus equisimilis.
XX  PN EP985729-A2.
XX  PD 15-MAR-2000.
XX
XX  13-AUG-1999; 99EP-0202639.
XX
XX  14-AUG-1998; 98CU-0000119.
XX
XX  (INGG-) CENT ING GENETICA & BIOTECNOLOGIA.
XX
XX  Torrens Madrazo IDC, Garcia Ojalvo A, De La Fuente Garcia JDJ;
XX  Seralena Menendez A;
XX  WPI; 2000-226041/20.
XX  DR N-PSDB; AA299251.
XX
XX  Recombinant production of streptokinase mutants, useful as thrombolytic
XX  agents for treating myocardial infarction, that are truncated at the N-
XX  or C-terminus -
XX
XX  Disclosure; Page 22-23; 54pp; English.
XX
XX  The present sequence represents a mutant protein of the streptokinase
XX  SKC-2. Streptokinase forms a complex with plasminogen, activating its
XX  conversion to plasmin. The SKC-2 gene was modified to produce the
XX  mutant protein. The obtained mutants conserve their capacity for
XX  plasminogen activator complex formation, thus having reduced
XX  antigenicity. The mutants are derived from the 1-1119 gene fragment,
XX  and retain the thrombolytic activity of SKC-2 but, compared with the
XX  full-length protein, are less antigenic and retain activity better in
XX  presence of antibodies that neutralize activity of the complete
XX  protein. The mutants are thrombolytic agents which are useful for
XX  treating myocardial infarction, pulmonary thromboembolism, surgical
XX  complications and other forms of thrombosis.
XX
XX  Sequence 372 AA;
XX
XX  Query Match 100.0%; Score 30; DB 21; Length 372;
XX  Best Local Similarity 100.0%; Pred. No. 68;
XX  Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX  QY 1 SVDVEY 6
XX  DB 157 SVDVEY 162
XX
XX  RESULT 22
XX  AA810198
XX  ID  AA810198 standard; Protein; 374 AA.
XX
XX  AA810198;
XX
XX  28-MAR-1991 (first entry)
XX
XX  Streptokinase(1-372, Lys 256, Lys 257 replaced by Lys-Pro-Lys-Pro).
XX  DE

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XX  streptokinase; thrombolytic agent; myocardial infarction.
XX
XX  Synthetic.
XX  PN EP407942-A.
XX
XX  16-JAN-1991.
XX
XX  09-JUL-1990; 90EP-0113099.
XX
XX  11-APR-1990; 90JP-0096830.
XX  PR 11-JUL-1989; 89JP-0179432.
XX  PR 27-NOV-1989; 89JP-0307957.
XX
XX  (SAKA ) OTSUKA PHARM FACTOR.
XX  Y:
XX  PI Majima E, Ogino K, Ono K, Sakata Y, Uenoyama T;
XX  WPI; 1991-016179/03.
XX
XX  Synthetic gene encoding streptokinase - scale, high purity prodn.
XX  of streptokinase used as a thrombolytic agent
XX
XX  Claim 10; Page 59; 76pp; English.
XX
XX  Streptokinase derivative having a C-terminal deletion (i.e. Pro
XX  373-Lys 414) and pro residues being inserted next to Lys at both
XX  positions 256 and 257. Derivatives show a decreased antigenicity,
XX  higher stability in blood and greater selectivity of thrombolytic
XX  activity and specificity. The protein is used as a thrombolytic
XX  agent in patients with lung thrombus or myocardial infarction.
XX  See also AAQ10230, AAR10195-7 and AAR10199-R10200.
XX
XX  Sequence 374 AA;
XX
XX  Query Match 100.0%; Score 30; DB 12; Length 374;
XX  Best Local Similarity 100.0%; Pred. No. 68;
XX  Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX  QY 1 SVDVEY 6
XX  DB 157 SVDVEY 162
XX
XX  RESULT 23
XX  AA84007
XX  ID  AA84007 standard; Protein; 384 AA.
XX
XX  AA84007;
XX
XX  03-JUL-2000 (first entry)
XX
XX  Amino acid sequence of a mutant streptokinase.
XX
XX  Streptokinase; SKC-2; plasminogen; plasmin; antigenicity;
XX  plasminogen activator complex formation; thrombolytic;
XX  myocardial infarction; pulmonary thromboembolism; thrombosis.
XX
XX  Synthetic.
XX  OS Streptococcus equisimilis.
XX  PN EP985729-A2.
XX
XX  15-MAR-2000.
XX
XX  13-AUG-1999; 99EP-0202639.
XX
XX  14-AUG-1998; 98CU-0000119.
XX
XX  (INGG-) CENT ING GENETICA & BIOTECNOLOGIA.
XX
XX  Torrens Madrazo IDC, Garcia Ojalvo A, De La Fuente Garcia JDJ;
XX  PI

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PI Seralena Menendez A;  
XX WPI; 2000-226041/20.  
DR N-PSDB; AA299252.  
XX  
PT Recombinant production of streptokinase mutants, useful as thrombolytic  
PT agents for treating myocardial infarction, that are truncated at the N-  
PT or C-terminus -  
XX  
XX  
PS Disclosure; Page 24-25; 54pp; English.  
XX  
XX The present sequence represents a mutant protein of the streptokinase  
CC SKC-2. Streptokinase forms a complex with plasminogen, activating its  
CC conversion to plasmin. The SKC-2 gene was modified to produce the  
CC mutant protein. The obtained mutants conserve their capacity for  
CC plasminogen activator complex formation, thus having reduced  
CC antigenicity. The mutants are derived from the 1-1119 gene fragment,  
CC and retain the thrombolytic activity of SKC-2 but, compared with the  
CC full-length protein, are less antigenic and retain activity better in  
CC presence of antibodies that neutralize activity of the complete  
CC protein. The mutants are thrombolytic agents which are useful for  
CC treating myocardial infarction, pulmonary thromboembolism, surgical  
CC complications and other forms of thrombosis.  
XX  
XX  
SQ Sequence 384 AA;  
Query Match 100.0%; Score 30; DB 21; Length 384;  
Best Local Similarity 100.0%; Pred. No. 70;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SVDVEY 6  
Db 157 SVDVEY 162  
|||||  
RESULT 24  
AAR10199  
ID AAR10199 standard; Protein; 391 AA.  
XX  
XX  
AC AAR10199;  
XX  
XX 28-MAR-1991 (first entry)  
XX  
XX Streptokinase (1-372, 45-68 deficient, Gln 256, Gln 257).  
DE  
XX streptokinase; thrombolytic agent; myocardial infarction.  
KW  
XX Synthetic.  
OS  
XX EP407942-A.  
PN  
XX 16-JAN-1991.  
PD  
XX 09-JUL-1990; 90EP-0113099.  
XX  
XX 11-APR-1990; 90JP-0096830.  
PR  
XX 11-JUL-1989; 89JP-0179432.  
PR  
XX 27-NOV-1989; 89UP-0307957.  
XX  
XX (SAKA ) OTSUKA PHARM FACTOR.  
PA  
XX  
XX Majima E, Ogino K, Ono K, Sakata Y, Uenoyama T;  
PI  
XX WPI; 1991-016179/03.  
DR  
XX Synthetic gene encoding streptokinase - scale, high purity prodn.  
PT Of streptokinase used as a thrombolytic agent  
PT  
XX  
XX Claim 11; Page 59; 76pp; English.  
PS  
XX Streptokinase derivative having a C-terminal deletion (i.e. Pro  
CC 373-Lys 414) and Arg 45 to Gly 68 also being deleted. In addition  
CC Gln residues replace Lys at positions 256 and 257. This is an

CC example of a streptokinase derivative which is a combination of two  
CC individually claimed modifications. Derivatives  
CC show a decreased antigenicity, higher stability in blood and greater  
CC selectivity of thrombolytic activity and specificity.  
CC The protein is used as a thrombolytic agent in  
CC patients with lung thrombus or myocardial infarction.  
CC See also AAQ10230, AAR10195-8 and AAR10200.  
XX  
XX  
SQ Sequence 391 AA;  
Query Match 100.0%; Score 30; DB 12; Length 391;  
Best Local Similarity 100.0%; Pred. No. 72;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SVDVEY 6  
Db 134 SVDVEY 139  
|||||  
RESULT 25  
AAY84004  
ID AAY84004 standard; Protein; 401 AA.  
XX  
XX AC AAY84004;  
XX  
XX 03-JUL-2000 (first entry)  
XX  
XX Amino acid sequence of a mutant streptokinase.  
DE  
XX Streptokinase; SKC-2; plasminogen; plasmin; antigenicity;  
KW plasminogen activator complex formation; thrombolytic;  
KW myocardial infarction; pulmonary thromboembolism; thrombosis.  
XX  
XX Synthetic.  
OS  
XX Streptococcus equisimilis.  
OS  
XX EP985729-A2.  
PN  
XX 15-MAR-2000.  
PD  
XX 13-AUG-1999; 99EP-0202639.  
PF  
XX 14-AUG-1998; 98CU-0000119.  
PR  
XX (INGG-) CENT ING GENETICA & BIOTECNOLOGIA.  
XX  
XX Torrens Madrazo IDC, Garcia Ojalvo A, De La Fuente Garcia JDU;  
PI Seralena Menendez A;  
PI  
XX WPI; 2000-226041/20.  
DR  
XX Recombinant production of streptokinase mutants, useful as thrombolytic  
PT agents for treating myocardial infarction, that are truncated at the N-  
PT or C-terminus -  
XX  
XX Disclosure; Page 18-20; 54pp; English.  
PS  
XX The present sequence represents a mutant protein of the streptokinase  
CC SKC-2. Streptokinase forms a complex with plasminogen, activating its  
CC conversion to plasmin. The SKC-2 gene was modified to produce the  
CC mutant protein. The obtained mutants conserve their capacity for  
CC plasminogen activator complex formation, thus having reduced  
CC antigenicity. The mutants are derived from the 1-1119 gene fragment,  
CC and retain the thrombolytic activity of SKC-2 but, compared with the  
CC full-length protein, are less antigenic and retain activity better in  
CC presence of antibodies that neutralize activity of the complete  
CC protein. The mutants are thrombolytic agents which are useful for  
CC treating myocardial infarction, pulmonary thromboembolism, surgical  
CC complications and other forms of thrombosis.  
XX  
XX  
SQ Sequence 401 AA;  
Query Match 100.0%; Score 30; DB 21; Length 401;

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Best Local Similarity 100.0%; Pred. No. 74;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVDVEY 6
Db 144 SVDVEY 149

RESULT 26
AAV25020
ID AAY25020 standard; peptide; 413 AA.
XX
AC AAY25020;
XX
DT 23-AUG-1999 (first entry)
DE Streptokinase fragment.
XX
KW Streptokinase; cell death; amelioration; treatment; disease; aging; AIDS;
KW cellular differentiation; physical insult; trauma; anoxia; hyperthermia;
KW hypothermia; brain; spinal cord; kidney; heart; lung; liver; skin; HIV;
KW viral disorder; hepatitis; retroviral; infection; encephalitis; FALS;
KW neurodegenerative disorder; Parkinson's disease; Alzheimer's disease;
KW Huntington's disease; cerebellar degeneration; cardiovascular disease;
KW familial amyotrophic lateral sclerosis; atherosclerosis; heart failure;
KW infarction; heart disease; cardiomyopathy; hypertensive; myocardial;
KW reperfusion injury; immune disease; rheumatoid arthritis; renal; retinal;
KW systemic lupus erythematosus; insulin-dependent; diabetes mellitus;
KW pernicious anemia; dermatomyositis; enychema nodosum; myasthenia gravis;
KW Sjogren's syndrome; temporal arthritis; autoimmune polyarthritides;
KW Wegener's granulomatosis; glomerulonephritis; anti-phospholipid syndrome;
KW neoplastic disorder; leukemia; sarcoma; myeloma; carcinoma; neuroma;
KW melanoma; cancer; breast; colon; cervix; prostate; Hodgkin's disease;
KW non-Hodgkin's lymphoma; inflammatory disorder; stroke; ischemia;
KW spinal cord; toxic insult; pulmonary; macular degeneration; cataract;
KW pancreatitis; Crohn's disease; ulcerative colitis; motor neuron disease;
KW Guillan Bare Syndrome; demyelinating disease; bypass surgery;
KW chemotherapy; clozapine; AZT; anthracycline.
XX
OS Unidentified.
XX
PN US5917013-A.
XX
PD 29-JUN-1999.
XX
PF 05-DEC-1996; 96US-0759599.
XX
PR 06-DEC-1995; 95US-0008233.
XX
PR 05-DEC-1996; 96US-0759599.
XX
PA (RASK/) RASKIN S W.
XX
PI Krystal G, Rabkin SW;
XX
DR WPI; 1999-394231/33.
XX
PT Peptides that ameliorate cell death useful for treating conditions
PT associated with cellular differentiation
XX
PS Disclosure; Fig 3; 15pp; English.
XX
CC AAY25009-Y25019 are novel peptides derived from streptokinase that
CC ameliorate cell death. The products of the invention and their encoding
CC nucleic acids may be useful for treating diseases and conditions related
CC to aging, cellular differentiation, physical insult (e.g. physical
CC trauma, anoxia, hyperthermia, hypothermia, chemically induced damage,
CC and trauma to the brain, spinal cord, kidney, heart, lungs, liver, skin
CC and any other organ), viral disorders (e.g. hepatitis, retroviral
CC infections, viral encephalitis, and AIDS/HIV), neurodegenerative
CC disorders (e.g. Parkinson's disease, Alzheimer's disease, Huntington's
CC disease, cerebellar degenerations, and familial amyotrophic lateral
CC sclerosis (FALS)), cardiovascular disease (e.g. atherosclerosis,
CC myocardial infarction, heart failure, cardiomyopathy, myocardial

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reperfusion injury, and hypertensive heart disease), immune disease (e.g.
rheumatoid arthritis, systemic lupus erythematosus, insulin-dependent,
diabetes mellitus, lupus, pernicious anaemia, dermatomyositis, enychema
nodosum, Sjogren's syndrome, temporal arthritis, myasthenia gravis,
Wegener's granulomatosis, glomerulonephritis, anti-phospholipid syndrome,
and autoimmune polyarthritides), a neoplastic disorder (e.g. leukemia,
sarcomas, myelomas, carcinomas, neuromas, melanoma, cancers of the
breast, brain, colon, cervix, and prostate, Hodgkin's disease and
non-Hodgkin's lymphoma), inflammatory disorders (e.g. inflammatory joint
disorders and inflammatory induced cell damage to the eye, brain and
other organs), ischemia or reperfusion injury (e.g. myocardial ischemia
and reperfusion injury, renal ischemia, spinal cord ischemia and/or
reperfusion injury, retinal ischemia or infarction, and stroke), toxic
insult (e.g. liver toxicity, pulmonary toxicity, toxic damage to other
organs from chemicals, radiation, and other noxious substances), macular
degeneration, cataract formation, pancreatitis, Crohn's disease,
ulcerative colitis, accelerated aging, spinal cord disease (e.g. motor
neuron diseases, degeneration of the spinal cord, Guillan Bare Syndrome
and demyelinating disease), bypass surgery, chemotherapy,
chemically-induced reperfusion, and therapeutics such as clozapine, AZT,
and anthracyclines.
XX
SQ Sequence 413 AA;
Query Match 100.0%; Score 30; DB 20; Length 413;
Best Local Similarity 100.0%; Pred No. 76;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVDVEY 6
Db 156 SVDVEY 161

RESULT 27
AAY84005
ID AAY84005 standard; protein; 413 AA.
XX
AC AAY84005;
XX
DT 03-JUL-2000 (first entry)
DE Amino acid sequence of a mutant streptokinase.
XX
KW Streptokinase; SKC-2; plasminogen; plasmin; antigenicity;
KW plasminogen activator complex formation; thrombolytic;
KW myocardial infarction; pulmonary thromboembolism; thrombosis.
XX
OS Synthetic.
OS Streptococcus equisimilis.
XX
PN EP985729-A2.
XX
PD 15-MAR-2000.
XX
PF 13-AUG-1999; 99EP-0202639.
XX
PR 14-AUG-1998; 98CU-0000119.
XX
PA (INGG-) CENT ING GENETICA & BIOTECNOLOGIA.
XX
PI Torrens Madrazo IDC, Garcia Ojalvo A, De La Fuente Garcia JDJ;
PI Seralena Menendez A;
XX
DR WPI; 2000-226041/20.
DR N-PSDB; AAZ99250.
XX
PT Recombinant production of streptokinase mutants, useful as thrombolytic
PT agents for treating myocardial infarction, that are truncated at the N-
PT or C-terminus
XX
PS Disclosure; Page 20-21; 54pp; English.
XX
CC The present sequence represents a mutant protein of the streptokinase

```

CC SKC-2. Streptokinase forms a complex with plasminogen, activating its  
 CC conversion to plasmin. The SKC-2 gene was modified to produce the  
 CC mutant protein. The obtained mutants conserve their capacity for  
 CC plasminogen activator complex formation, thus having reduced  
 CC antigenicity. The mutants are derived from the 1-119 gene fragment,  
 CC and retain the thrombolytic activity of SKC-2 but, compared with the  
 CC full-length protein, are less antigenic and retain activity better in  
 CC presence of antibodies that neutralize activity of the complete  
 CC protein. The mutants are thrombolytic agents which are useful for  
 CC treating myocardial infarction, pulmonary thromboembolism, surgical  
 CC complications and other forms of thrombosis.

XX Sequence 413 AA;

Query Match 100.0%; Score 30; DB 21; Length 413;

Best Local Similarity 100.0%; Pred. No. 76;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVEY 6

Db 144 SVDVEY 149

RESULT 28

ABB80012  
 ID ABB80012 standard; protein; 413 AA.

XX AC ABB80012;

XX DT 26-JUL-2002 (first entry)

XX DE Streptokinase amino acid sequence.

XX Streptokinase; cell death; apoptosis; necrosis; neutropenic; neutropenic;  
 KW neuroprotective; antiparkinsonian; anticonvulsant; cytostatic;  
 KW antiinflammatory; antihistaminic; antirheumatic; cardiant;  
 KW antithrombotic; vasotropic; immunosuppressive; anti-HIV;  
 KW dermatological; antidiabetic; antianaemic; virucide; ophthalmological;  
 KW antitumor; antibacterial; antiparasitic; neurodegenerative disease;  
 KW Parkinson's disease; Alzheimer's disease; Huntington's disease;  
 KW cerebellar degeneration; neoplastic disorder; cancer;  
 KW inflammatory disorder; arthritis; inflammatory joint disorders;  
 KW cardiovascular disease; heart failure; atherosclerosis;  
 KW myocardial reperfusion injury; immune disease; autoimmune disease;  
 KW acquired immunodeficiency syndrome; AIDS; rheumatoid arthritis;  
 KW systemic lupus erythematosus; diabetes mellitus; pernicious anaemia;  
 KW myelodysplastic diseases; viral diseases; macular degeneration;  
 KW cataract; Crohn's disease; ulcerative colitis; pancreatitis;  
 KW prion disease; aging.

XX Synthetic.

XX US6348567-B1.

XX PD 19-FEB-2002.

PF 19-APR-1999; 99US-0294457.

PR 06-DEC-1995; 95US-008233P.

PR 05-DEC-1996; 96US-0759599.

XX (MOLE-) MOLECULAR THERAPEUTICS INC.

XX Krystal G, Rabkin SW;

XX WPI; 2002-266542/31.

XX New peptides obtained from streptokinase, useful in ameliorating cell  
 PT death due to apoptosis and/or necrosis and treating neurodegenerative,  
 PT neoplastic, immune, cardiovascular and inflammatory disorders -  
 XX Disclosure; Fig 3; 18pp; English.

CC The invention relates to an isolated peptide obtained from streptokinase,  
 CC or its derivative or analog, which ameliorate cell death. The activity of  
 CC peptides of the invention may be described as, neurotropic,  
 CC neuroprotective, antiparkinsonian, anticonvulsant, cytostatic,  
 CC antiinflammatory, antihistaminic, antirheumatic, cardiant,  
 CC antithrombotic, vasotropic, immunosuppressive, anti-HIV,  
 CC dermatological, antidiabetic, antianaemic, virucide, ophthalmological,  
 CC antitumor, antibacterial and antiparasitic. Peptides of the invention  
 CC ameliorates apoptosis and necrosis in a warm-blooded animal. Compositions  
 CC comprising peptides of the invention are useful for treating  
 CC neurodegenerative diseases (e.g. Parkinson's, Alzheimer's, Huntington's  
 CC disease and cerebellar degeneration) neoplastic disorders including  
 CC cancer, inflammatory disorders (e.g. arthritis, inflammatory joint  
 CC disorders), cardiovascular diseases (e.g. heart failure, atherosclerosis  
 CC disease, acquired immunodeficiency syndrome (AIDS), rheumatoid arthritis,  
 CC systemic lupus erythematosus, diabetes mellitus, pernicious anaemia),  
 CC myelodysplastic diseases, viral diseases, and degenerative diseases of  
 CC any organ. Other disorders include macular degeneration, cataracts,  
 CC Crohn's disease, ulcerative colitis, cataracts, pancreatitis, infectious  
 CC diseases including bacteria, parasite, prion-based diseases, and  
 CC accelerated aging. The current sequence represents a representative  
 CC streptokinase amino acid sequence.

XX Sequence 413 AA;

Query Match 100.0%; Score 30; DB 23; Length 413;

Best Local Similarity 100.0%; Pred. No. 76;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVEY 6

Db 156 SVDVEY 161

RESULT 29

ABG74199

ID ABG74199 standard; Protein; 413 AA.

XX AC ABG74199;

XX DT 06-MAY-2003 (first entry)

XX DE Representative streptokinase sequence.

XX Cell death; streptokinase; neurodegenerative disorder; leukaemia; AIDS;  
 KW Parkinson's disease; Alzheimer's disease; cardiovascular disease; trauma;  
 KW atherosclerosis; myocardial infarction; immune disease; carcinoma;  
 KW rheumatoid arthritis; neoplastic disorder; inflammatory disorder;  
 KW arthritis; inflammatory induced cell damage; motor neuron disease;  
 KW physical insult; severe shock; ischaemia; reperfusion injury; hepatitis;  
 KW cell death associated procedure; spinal cord reperfusion injury;  
 KW toxic insult; liver toxicity; pulmonary toxicity; spinal cord disease;  
 KW Guillain-Barre syndrome; bypass surgery; myocardial ischaemia;  
 KW chemotherapy; viral disease; viral encephalitis; infectious disease;  
 KW bacterial disease; prion-based disease; macular degeneration;  
 KW cataract formation; pancreatitis; Crohn's disease; ulcerative colitis;  
 KW accelerated aging; oxidative stress.

XX Unidentified.

XX Key Location/Qualifiers

FT Peptide 156..161

FT /label= 6mer peptide #1

FT /note= "Cell death ameliorating peptide. Specifically

FT claimed in claim 2"

FT Peptide 156..171

FT /label= 18mer peptide

FT /note= "Cell death ameliorating peptide. Specifically

FT claimed in claim 2. This is SEQ ID NO 5 as shown

FT in the sequence listing"

FT Peptide 156..173

FT /label= 18mer peptide

FT /note= "Cell death ameliorating peptide. Specifically  
FT claimed in claim 2. This is SEQ ID NO 5 as shown  
FT on page 8"  
FT  
FT Peptide 156..176  
FT /label= Fraction 13\_peptide  
FT /note= "Cell death ameliorating peptide. Specifically  
FT claimed in claim 2"  
FT  
FT Peptide 299..304  
FT /label= 6mer peptide #2  
FT /note= "Cell death ameliorating peptide. Specifically  
FT claimed in claim 2"  
FT  
FT Peptide 299..309  
FT /label= 11mer peptide  
FT /note= "Cell death ameliorating peptide. Specifically  
FT claimed in claim 2"  
FT  
FT Peptide 299..318  
FT /label= Fraction 12\_peptide  
FT /note= "Cell death ameliorating peptide. Specifically  
FT claimed in claim 2"  
FT  
XX US2002165129-A1.  
XX  
XX 07-NOV-2002.  
XX  
XX 31-JUL-2001; 2001US-0919703.  
XX  
XX 06-DEC-1995; 95US-008233P.  
XX  
XX 19-APR-1999; 99US-0294457.  
XX  
XX 03-DEC-1996; 96US-0759599.  
XX  
XX (KRYSTAL G.  
XX (RABKIN S W.  
XX  
XX Krystal G, Rabkin SW;  
XX  
XX WPI; 2003-246673/25.  
XX  
XX Pharmaceutical composition for treating e.g. neurodegenerative  
XX disorder, cardiovascular disease, neoplastic disorder, viral disease  
XX and immune diseases, comprises a peptide capable of ameliorating cell  
XX death  
XX  
XX Disclosure; Fig 3; 19pp; English.  
XX  
XX The invention relates to a pharmaceutical composition, which comprises a  
XX peptide capable of ameliorating cell death, its derivative or analogue,  
XX comprising a sequence Val-Asp-Val, where the peptide is in a suitable  
XX pharmaceutical carrier or diluent. The pharmaceutical composition  
XX (comprising the peptide) is useful for treating or preventing cell  
XX death associated with a neurodegenerative disorder e.g. Parkinson's  
XX disease and Alzheimer's disease; cardiovascular disease e.g.  
XX atherosclerosis and myocardial infarction; immune disease e.g. AIDS and  
XX rheumatoid arthritis; neoplastic disorders e.g. leukaemia and carcinoma;  
XX inflammatory disorder e.g. arthritis and inflammatory induced cell  
XX damage; disease caused by physical insult e.g. trauma and severe shock;  
XX ischaemia or reperfusion injury e.g. myocardial ischaemia and spinal cord  
XX reperfusion injury; toxic insult e.g. liver toxicity and pulmonary  
XX toxicity; spinal cord disease e.g. motor neuron disease and Guillain-Barré  
XX syndrome; procedures associated with cell death e.g. bypass surgery and  
XX chemotherapy; viral disease e.g. hepatitis and viral encephalitis;  
XX infectious diseases e.g. bacterial disease and prion-based disease;  
XX macular degeneration; cataract formation; pancreatitis; Crohn's disease;  
XX ulcerative colitis; accelerated aging and oxidative stress in a warm-  
XX blooded animal. The present sequence represents the amino acid sequence  
XX of a representative streptokinase from which the cell death ameliorating  
XX peptides are produced.  
XX  
XX Sequence 413 AA;

Query Match 100.0%; Score 30; DB 24; Length 413;  
Best Local Similarity 100.0%; Pred. No. 76;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVEY 6  
Db 156 SVDVEY 161  
  
RESULT 30  
AAR10194  
ID AAR10194 standard; Protein; 414 AA.  
XX  
XX AAR10194;  
AC AAR10194;  
XX  
XX 28-MAR-1991 (first entry)  
DT  
XX  
XX Streptokinase encoded by synthetic gene.  
DE  
XX  
XX streptokinase; thrombolytic agent; myocardial infarction.  
KW  
XX  
XX Synthetic.  
OS  
XX  
XX EP407942-A.  
PN  
XX  
XX 16-JAN-1991.  
PD  
XX  
XX 09-JUL-1990; 90EP-0113099.  
PF  
XX  
XX 11-APR-1990; 90JP-0096830.  
PR  
XX  
XX 11-JUL-1989; 89JP-0179432.  
PR  
XX  
XX 27-NOV-1989; 89JP-0307957.  
PR  
XX  
XX (SAKA ) OTSUKA PHARM FACTOR.  
PA  
XX  
XX  
XX Majima E, Ogino K, Ono K, Sakata Y, Uenoyama T;  
PI  
XX  
XX WPI; 1991-016179/03.  
DR  
XX  
XX N-PSDB; AAQ10230.  
DR  
XX  
XX Synthetic gene encoding streptokinase - scale, high purity prodn.  
PT  
XX  
XX of streptokinase used as a thrombolytic agent  
PT  
XX  
XX Claim 1; Page 51; 76pp; English.  
PS  
XX  
XX Streptokinase and its derivatives can be produced in large  
CC quantities with high purity for use as thrombolytic agents in  
CC patients with lung thrombus or myocardial infarction.  
CC See also AAR10195-R10200.  
CC  
XX  
XX Sequence 414 AA;  
SQ  
  
Query Match 100.0%; Score 30; DB 12; Length 414;  
Best Local Similarity 100.0%; Pred. No. 76;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 SVDVEY 6  
Db 157 SVDVEY 162  
  
RESULT 31  
AAR20202  
ID AAR20202 standard; Protein; 414 AA.  
XX  
XX AAR20202;  
AC AAR20202;  
XX  
XX 25-MAR-2003 (updated)  
DT  
XX  
XX 21-APR-1992 (first entry)  
DT  
XX  
XX S.equisimilis streptokinase.  
DE  
XX  
XX plasminogen activator; coronary thrombosis; ATCC-9542.  
KW  
XX  
XX Streptococcus equisimilis.  
OS  
XX  
XX AU9178101-A.  
PN



```
XX      28-NOV-1991.
XX PD
XX XX
XX PF          91AU-0078101.
XX PR
XX PP          90CU-0000090.
XX PA
XX PPA        (INGG-) CENT ING GENETICA & BIOTECNOLOGIA.
XX PI Garcia MPE, Chaplen RR, Hidalgo AP, Doce RS, Marrero LFH;
XX PPI Collozzo PR, Ramirez AC, Munoz EAM, Martinez WB, Somavilla MC;
XX PPI Fernandez AP, Garcia J, Martinez LSH,
XX XX WPI; 1992-024716/04.
XX DR N-PSDB; AAQ20665.
XX DR
XX XX Streptokinase C-2 gene from S.equisimilis type C - plasmids and
XX PT transformants for large scale intra- and extracellular expression
XX PPT of SKC-2 useful in thrombolytic agents
XX XX Claim 13; Page 14; 28pp; English.
XX PS The SKC-2 gene was isolated from S.equisimilis type C by gene
XX CC amplification from the synthetic primers SK1, SK2 and SK3 (see
CC AAQ20666-8). The SKC-2 gene was inserted into yeast expression vector
CC CCS pPS-7 for intracellular expression of streptokinase and into pNAO
CC CC for intracellular expression in yeast. For expression in bacteria,
CC CC the SKC-2 gene was inserted in plamid pEKG3, between a trp promoter
CC CC and a T4 terminator.
XX CC (Updated on 25-MAR-2003 to correct PA field.)
XX CS Sequence 414 AA;
XX SQ
Query Match           100.0%; Score 30; DB 13; Length 414;
Best Local Similarity   100.0%; Pred. No. 76;
Matches    6; Conservative     0; Mismatches    0; Indels    0; Gaps    0;
QY       1 SDVEYE 6
         |||||
Db        157 SDVEYE 162
RESULT 32
AAR63120
ID AAR63120 standard; protein; 414 AA.
AC AAR63120;
XX XX
XX DT 25-MAR-2003 (updated)
DT DT 16-NOV-1994 (first entry)
XX DE Streptokinase.
XX ST Streptokinase; SK; Streptococcus equisimilis; plasminogen;
KW myocardial infarction.
XX OS Streptococcus equisimilis.
XX FH Location/Qualifiers
FT Region 14..414
FT /note= "claim 1, see CC"
FT Region 244..352
FT /note= "claim 2, see CC"
FT Region 1...352
FT /note= "claim 3, see CC"
FT Region 120..352
FT /note= "claim 3, see CC"
FT Region 244..414
FT /note= "claim 3, see CC"
XX PN WO9407992-A1.
XX PD 14-APR-1994.
```

XX	05-OCT-1993;	93WO-US09502.	
XX	05-OCT-1992;	92US-0956692.	
XX	29-SEP-1993;	93US-0128299.	
XX	(GEO ) GEN HOSPITAL CORP.		
XX	(HARD ) HARVARD COLLEGE.		
XX	Reed GL;		
XX	WPI; 1994-135561/16.		
XX	DNA encoding a polypeptide which binds to plasminogen and		
XX	corresponds to region of streptokinase - useful to detect		
XX	plasminogen in a sample and to treat myocardial infarction		
XX	Dislosure; Page 40-41; 52pp; English.		
XX	Nucleic acid comprising a sequence encoding amino acids		
XX	14-414 of streptokinase, which binds to plasminogen and does		
XX	not have a sequence comprising amino acids 60-414 is new.		
XX	The polypeptide pref. comprises amino acids 244-352, 1-352,		
XX	120-352 or 244-414.		
XX	CC (Updated on 25-MAR-2003 to correct PN field.)		
XX	Sequence 414 AA;		
XX	Query Match 100.0%; Score 30; DB 15; Length 414;		
XX	Best Local Similarity 100.0%; Pred. No. 76;		
XX	Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps		
XX	1 SVDVEY 6		
XX	157 SVDVEY 162		
XX	RESULT 33		
XX	RAY24794		
XX	ID RAY24794 standard; Protein; 414 AA.		
XX	AC RAY24794;		
XX	26-AUG-1999 (first entry)		
XX	Streptococcus equisimilis native streptokinase.		
XX	Streptococcus; streptokinase; fibrin-dependent plasminogen activator;		
XX	nsk; rsk; bacterial; blood clot; thrombotic condition;		
XX	myocardial infarction; venous thrombosis; pulmonary embolism;		
XX	cerebral thrombosis; graft thrombosis; arterial thrombosis.		
XX	Streptococcus equisimilis.		
XX	W09931247-A1.		
XX	24-JUN-1999.		
XX	15-DEC-1998; 98WO-US26694.		
XX	15-DEC-1997; 97US-0069497.		
XX	(HARD ) HARVARD COLLEGE.		
XX	Reed GL;		
XX	WPI; 1999-395183/33.		
XX	N-PSDB; RAX80492.		
XX	N-terminally deleted streptokinase		
XX	Claim 30; Page 60-61; 73pp; English.		

CC The present invention describes an isolated bacterial protein that  
 CC induces fibrin-dependent plasminogen activation in a pharmaceutical  
 CC composition for dissolving blood clots. Also described are: (1) a  
 CC composition comprising an isolated modified streptokinase, the  
 CC modification being removal of amino acid residues in the amino terminus;  
 CC (2) a method for dissolving a blood clot in a subject, comprising  
 CC administering to the subject a fibrin-dependent streptokinase protein;  
 CC a nucleic acid (I) encoding a modified bacterial streptokinase; (3) an  
 CC expression vector comprising (I); and (4) a host cell transformed with  
 CC the expression vector of (3). The pharmaceutical composition comprising  
 CC a bacterial fibrin-dependent plasminogen activator is useful for  
 CC dissolving blood clots in patients with a thrombotic condition, e.g.  
 CC myocardial infarction, venous thrombosis, pulmonary embolism, cerebral  
 CC thrombosis, graft thrombosis and arterial thrombosis. The modified  
 CC streptokinase can also be used in non-human mammals. Streptokinase  
 CC activation of plasminogen is at least 10-fold, preferably 100-fold  
 CC greater in the presence of fibrin than in the absence of fibrin. The  
 CC modified streptokinase has at least one amino acid substitution that  
 CC inactivates a substrate site for proteolytic cleavage. This reduces the  
 CC rate of degradation of the streptokinase at least two-fold. The present  
 CC sequence represents native streptokinase (nsk).

XX SQ Sequence 414 AA;  
 Query Match 100.0%; Score 30; DB 20; Length 414;  
 Best Local Similarity 100.0%; Pred. No. 76;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVDVEY 6  
 |||||  
 Db 157 SVDVEY 162

RESULT 34  
 AAY01556  
 ID AAY01556 standard; peptide; 414 AA.

XX AC AAY01556;

XX DT 18-JUN-1999 (first entry)

XX DE Native streptokinase protein sequence.

XX KW Antigenic peptide; streptokinase; streptokinase-specific antibody;  
 XX thrombolytic activity; thrombolytic therapy; glomerulonephritis;  
 XX rheumatic fever.

XX OS Streptococcus equisimilis.

XX PN W09908698-A1.

XX PD 25-FEB-1999.

XX PF 18-AUG-1998; 98WO-US17114.

XX PR 18-AUG-1997; 97US-0055911.

XX PA (GEO ) GEN HOSPITAL CORP.  
 XX (HARD ) HARVARD COLLEGE.

XX PI Parhami-Seren B, Reed GL;

XX XX WPI; 1999-190113/16.

XX PT New polypeptides which bind streptokinase-specific antibodies -  
 XX useful in thrombolytic therapy

XX PS Disclosure; Page 12; 44pp; English.

XX CC The present sequence represents a native streptokinase. The  
 CC specification describes a polypeptide which binds to a  
 CC streptokinase-specific antibody and prevents the antibody  
 CC binding to native streptokinase. The specification also

CC describes a synthetic polypeptide (PI) comprising an epitope  
 CC which binds to an streptokinase-specific antibody and reduces  
 CC thrombolytic activity of streptokinase. PI is used in thrombolytic  
 CC therapy, and to prevent or treat glomerulonephritis and rheumatic  
 CC fever.

XX SQ Sequence 414 AA;

Query Match 100.0%; Score 30; DB 20; Length 414;

Best Local Similarity 100.0%; Pred. No. 76;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVDVEY 6

Db 157 SVDVEY 162

RESULT 35

AAW94664

ID AAW94664 standard; Protein; 414 AA.

XX AC AAW94664;

XX DT 04-MAY-1999 (first entry)

XX DE Streptococcus equisimilis native streptokinase.

XX KW Streptococcus equisimilis H46A; streptokinase; mutant; fibrinolytic;

XX KW plasma clot; hydrolysis; haemolytic Streptococcus; plasminogen;

XX KW plasmin; serine protease; fibrin; blood clot; thrombolytic;

XX KW vascular thromboembolytic symptom; acute myocardial infarction;

XX KW fibrinolysis; resistance.

XX OS Streptococcus equisimilis.

XX FH Key Location/Qualifiers

XX FT Misc-difference 14

XX PT /note= "encoded by ACC"

XX PN US5876999-A.

XX PD 02-MAR-1999.

XX PF 06-DEC-1995; 95US-0568393.

XX PR 06-DEC-1995; 95US-0568393.

XX PA (NASC-) NAT SCI COUNCIL.

XX PI Wu H;

XX DR WPI; 1999-189643/16.

XX DR N-PSDB; AAX16632.

XX PT Mutant streptokinase polypeptide - useful as plasmin-resistant

XX PT thrombolytic agent

XX PS Claim 1; Column 7-10; 17pp; English.

XX CC The present invention describes a mutant streptokinase (SK) polypeptide  
 CC in which at least one of the amino acids in the Pro58-Lys59-Ser60-Lys61  
 CC segment of the corresponding native SK is replaced by another amino acid.  
 CC The present sequence represents native SK. SK is a secretory protein of  
 CC haemolytic Streptococcus able to activate human plasminogen (HPIg) to  
 CC plasmin (HPI), which is a serine protease able to catalyze the  
 CC hydrolysis of fibrin in blood clots. The SK is useful as a thrombolytic  
 CC agent in the treatment of vascular thromboembolytic symptoms such as  
 CC acute myocardial infarction. Compared with wild-type SK, the K59E mutant  
 CC is more resistant to degradation by human plasmin and is more effective  
 CC both in acting as a fibrinolytic agent and in activating human plasminogen.

XX SQ Sequence 414 AA;

The invention relates to a method for the production of non-immunogenic proteins. The method comprises determining at least part of the amino acid sequence of the protein; b) identifying in the amino acid sequence one or more potential epitopes for T-cells (T-cell epitopes) of the given species; and (c) modifying the amino acid sequence to eliminate at least one of the T-cell epitopes identified in step (b) thereby to eliminate or reduce the immunogenicity of the protein when exposed to the immune system of the given species. A method of analysing a pre-existing protein to predict the basis for immunogenic responses is also provided. The methods can be used particularly for reducing the immunogenicity of immunoglobulins or therapeutic proteins, e.g. Streptokinase (SK). The products can be used for diagnosis and therapy. The present sequence represents the amino acid sequence of the SK protein.

XX DE De-immunised streptokinase (SK) protein sequence.  
XX KW Non-immunogenic; epitope; T-cell; immunogenicity; immune system; SK;  
XX KW immunogl bulin; therapeutic; streptokinase; de-immunised.  
XX OS Streptococcus equisimilis.  
XX PN WC9852976-A1.  
XX PD 26-NOV-1998.  
XX PF 21-MAY-1998; 98MO-GB01473.  
XX PR 14-APR-1998; 98GB-0007751.  
XX PR 21-MAY-1997; 97GB-0010480.  
XX PR 31-JUL-1997; 97GB-0016197.  
XX PR 28-NOV-1997; 97GB-0025270.  
XX PR 02-DEC-1997; 97US-0067235.  
XX PA (BIOV-) BIOVATION LTD.  
XX PI Carr FJ;  
XX PX WPI; 1999-045301/04.  
XX PT Reducing immunogenicity of proteins - by modifying the amino acid  
XX PT sequence of the protein to eliminate potential epitopes for T-cells  
XX PT of a given species  
XX PS Example 6; Fig 29; 77pp; English.  
XX CC The invention relates to a method for the production of non-immunogenic  
XX CC proteins. The method comprises determining at least part of the amino  
XX CC acid sequence of the protein; (b) identifying in the amino acid sequence  
XX CC one or more potential epitopes for T-cells (T-cell epitopes) of the given  
XX CC species; and (c) modifying the amino acid sequence to eliminate at least  
XX CC one of the T-cell epitopes identified in step (b) thereby to eliminate or  
XX CC reduce the immunogenicity of the protein when exposed to the immune  
XX CC system of the given species. A method of analysing a pre-existing protein  
XX CC to predict the basis for immunogenic responses is also provided. The  
XX CC methods can be used particularly for reducing the immunogenicity of  
XX CC immunoglobulins or therapeutic proteins, e.g. Streptokinase (SK). The  
XX CC products can be used for diagnosis and therapy. The present sequence  
XX CC represents the amino acid sequence of a de-immunised SK protein molecule.  
XX SQ Sequence 414 AA;  
Query Match 100.0%; Score 30; DB 20; Length 414;  
Best Local Similarity 100.0%; Pred. No. 76;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SVDVEY 6  
Db 157 SVDVEY 162  
RESULT 39  
AAY90282  
ID AAY90282 standard; Protein; 414 AA.  
XX AC AAY90282;  
XX DT 13-OCT-2000 (first entry)  
XX DE S. equisimilis streptokinase.  
XX KW Streptokinase; SK; hybrid plasminogen activator; fibrin binding region;  
XX KW plasminogen; human; fibrinectin; thrombolytic therapy;  
XX KW cardiovascular disorder; fibrinectin.  
XX OS Streptococcus equisimilis.

PN EF1024192-A2.  
XX PD 02-AUG-2000.  
XX PF 23-DEC-1999; 99BP-0310541.  
XX PR 24-DEC-1998; 98IN-0003825.  
XX PA (COUL ) CSIR COUNCIL SCI IND RES.  
XX PI Sahni G, Kumar R, Roy C, Rajogopal K, Nihalani D, Sundaram V;  
XX PI Yadav M;  
XX DR WPI; 2000-516032/47.  
XX DR N-PSDB; AAA37633.  
XX PT Hybrid streptokinase-fibrin binding domain polypeptides useful for  
XX PT thrombolytic therapy comprises a streptokinase fused with fibrin  
XX PT binding domains of human fibrinectin -  
XX PS Example 3; Fig 3; 58pp; English.  
XX CC This sequence represents the human Streptococcus equisimilis  
XX CC streptokinase protein sequence. The invention relates to a hybrid  
XX CC plasminogen activator (PA) comprises a polypeptide fusion between  
XX CC streptokinase (SK), which are capable of plasminogen (PG) activation,  
XX CC and fibrin binding regions of human fibrinectin, which are from fibrin  
XX CC binding domains (Rgp) 4 and 5 or 1 and 2. The hybrid PA possesses the  
XX CC ability to bind with fibrin independently and also characteristically  
XX CC retains a PG activation ability which becomes evident only after a  
XX CC pronounced duration, or lag, after exposure of the PA to a suitable  
XX CC animal or human PG. The hybrid streptokinase-fibrin binding domain  
XX CC polypeptides are useful in thrombolytic therapy for various kinds of  
XX CC cardiovascular disorders. The hybrids have enhanced fibrin selectivity as  
XX CC well as kinetics of plasminogen activation that are distinct from that of  
XX CC natural streptokinase in being characterised by a temporary delay, or  
XX CC lag of several minutes in the natural rate of the catalytic conversion  
XX CC of plasminogen to plasmin (i.e. delayed-action thrombolysis). The  
XX CC proteins can bind tightly with fibrin in blood clots soon after  
XX CC introduction into the vascular system without significantly activating  
XX CC the circulating blood plasminogen to plasmin, thus aiding in the  
XX CC localisation of the plasminogen activation process to the site of  
XX CC pathological thrombus. This overcomes systemic plasminogen activation  
XX CC encountered during clinical use of streptokinase.  
XX SQ Sequence 414 AA;  
Query Match 100.0%; Score 30; DB 21; Length 414;  
Best Local Similarity 100.0%; Pred. No. 76;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SVDVEY 6  
Db 157 SVDVEY 162  
RESULT 40  
AAB01295  
ID AAB01295 standard; protein; 414 AA.  
XX AC AAB01295;  
XX DT 25-SEP-2000 (first entry)  
XX DE Wild type streptokinase from Streptococcus equisimilis.  
XX KW Immunogenicity; immunogen; T cell epitope; T-lymphocyte; drug;  
XX KW vaccine; carrier; diagnosis; therapy; complement; C3; C5; CVP;  
XX KW plasminogen; streptokinase; fibrin; blood clot; thrombolysis;  
XX KW plasmin; myocardial infarction.  
XX OS Streptococcus equisimilis.

PN WO200034317-A2.  
XX 15-JUN-2000.  
XX 08-DEC-1999; 99WO-GB04119.  
XX 08-DEC-1998; 98GB-0026925.  
PR 02-FEB-1999; 99GB-0002139.  
XX (BIOV-) BIOVATION LTD.  
XX Carr FU, Adair FS, Hamilton AA, Carter G;  
XX WPI; 2000-423372/36.  
XX  
XX Rendering a protein non-immunogenic or less immunogenic useful in  
PT medicine and in diagnostics involves determining the amino acid  
PT sequence of the protein, identifying and modifying potential epitopes  
XX  
XX Example 2; Fig 5; 42pp; English.  
XX  
XX Proteins or their fragments can be rendered non-immunogenic or less  
CC immunogenic by identifying one or more potential T cell epitopes and  
CC modifying the sequence to eliminate at least one of these T cell  
CC epitopes to reduce the immunogenicity of the protein when exposed to  
CC the immune system of another organism. The method can be used for  
CC producing a protein with an enzymatic activity which has a beneficial  
CC therapeutic effect, a protein used to convert inactive drugs to its  
CC active form within a living organism, a vaccine, a protein used as a  
CC carrier of other molecule or a protein which binds to other molecules  
CC within or introduced within the living organism in order to alter the  
CC bio distribution of other molecules, such that the protein does not  
CC stimulate immune response in the living organism. The less immunogenic  
CC protein is useful in medicine, diagnosis and in manufacture of a  
CC therapeutic or a diagnostic agent. Streptokinase is produced by  
CC certain strains of beta-haemolytic streptococci. The protein has no  
CC inherent enzymatic activity but has considerable clinical importance  
CC owing to its ability to efficiently bind human plasminogen,  
CC potentiating its activation to plasmin and thereby promoting the  
CC dissolution of fibrin filaments in blood clots. Streptokinase is an  
CC effective thrombolytic agent in the treatment of coronary thrombosis,  
CC improving survival and preserving left ventricular function following  
CC myocardial infarction. The native protein is immunogenic and the  
CC production of neutralising antibodies in humans generally limits the  
CC protein to a single use. The new method could provide a longer  
CC therapeutic use for streptokinase. This is the sequence  
CC of the wild type streptokinase. The altered streptokinase sequence  
CC is given in AAB01296. See GENESQ records AAB01289-B01302.  
XX  
XX Sequence 414 AA;  
SQ  
Query Match 100.0%; Score 30; DB 21; Length 414;  
Best Local Similarity 100.0%; Pred. No. 76;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SVDVEY 6  
Db 157 SVDVEY 162  
RESULT 41  
AAB01296  
ID AAB01296 standard; protein; 414 AA.  
XX AAB01296;  
AC  
XX 25-SEP-2000 (first entry)  
XX Altered streptokinase from Streptococcus equisimilis.  
XX  
XX Immunogenicity; immunogen; T cell epitope; T-lymphocyte; drug;  
KW vaccine; carrier; diagnosis; therapy; complement; C3; C5; C6F;  
KW plasminogen; streptokinase; fibrin; blood clot; thrombolysis;  
KW

KW plasmin; myocardial infarction.  
XX  
XX Synthetic.  
OS Streptococcus equisimilis.  
XX  
XX WO200034317-A2.  
XX  
XX 15-JUN-2000.  
PD  
XX 08-DEC-1999; 99WO-GB04119.  
XX 08-DEC-1998; 98GB-0026925.  
PR 02-FEB-1999; 99GB-0002139.  
XX (BIOV-) BIOVATION LTD.  
XX Carr FU, Adair FS, Hamilton AA, Carter G;  
XX WPI; 2000-423372/36.  
XX  
XX Rendering a protein non-immunogenic or less immunogenic useful in  
PT medicine and in diagnostics involves determining the amino acid  
PT sequence of the protein, identifying and modifying potential epitopes  
XX  
XX Example 2; Fig 6; 42pp; English.  
XX  
XX Proteins or their fragments can be rendered non-immunogenic or less  
CC immunogenic by identifying one or more potential T cell epitopes and  
CC modifying the sequence to eliminate at least one of these T cell  
CC epitopes to reduce the immunogenicity of the protein when exposed to  
CC the immune system of another organism. The method can be used for  
CC producing a protein with an enzymatic activity which has a beneficial  
CC therapeutic effect, a protein used to convert inactive drugs to its  
CC active form within a living organism, a vaccine, a protein used as a  
CC carrier of other molecule or a protein which binds to other molecules  
CC within or introduced within the living organism in order to alter the  
CC bio distribution of other molecules, such that the protein does not  
CC stimulate immune response in the living organism. The less immunogenic  
CC protein is useful in medicine, diagnosis and in manufacture of a  
CC therapeutic or a diagnostic agent. Streptokinase is produced by  
CC certain strains of beta-haemolytic streptococci. The protein has no  
CC inherent enzymatic activity but has considerable clinical importance  
CC owing to its ability to efficiently bind human plasminogen,  
CC potentiating its activation to plasmin and thereby promoting the  
CC dissolution of fibrin filaments in blood clots. Streptokinase is an  
CC effective thrombolytic agent in the treatment of coronary thrombosis,  
CC improving survival and preserving left ventricular function following  
CC myocardial infarction. The native protein is immunogenic and the  
CC production of neutralising antibodies in humans generally limits the  
CC protein to a single use. The new method could provide a longer  
CC therapeutic use for streptokinase. This is the sequence  
CC of the altered streptokinase. The wild type streptokinase sequence  
CC is given in AAB01295. See GENESQ records AAB01289-B01302.  
XX  
XX Sequence 414 AA;  
SQ  
Query Match 100.0%; Score 30; DB 21; Length 414;  
Best Local Similarity 100.0%; Pred. No. 76;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SVDVEY 6  
Db 157 SVDVEY 162  
RESULT 42  
AAB74940  
ID AAB74940 standard; protein; 414 AA.  
XX AAB74940;  
AC  
XX 02-JUL-2001 (first entry)  
XX

DE Mutant streptokinase protein sequence K59E.  
XX Streptokinase; mutant; human; plasmin; plasminogen; thrombolytic.  
KW Unidentified.  
OS

XX Key Location/Qualifiers  
FH Misc-difference 59 /note= "Lys in wild type sequence"  
FT Misc-difference 127 /label= unknown  
FT Misc-difference 370 /label= unknown  
FT /notes= "given as being encoded by NNN due to poor  
quality text"  
FT /label= unknown  
FT /notes= "given as being encoded by NNN due to poor  
quality text"

XX TW416990-A.  
XX  
XX 01-JAN-2001.  
XX  
XX 11-JUL-1995; 95TW-0107238.  
XX  
XX 11-JUL-1995; 95TW-0107238.  
XX  
XX (NASC-) NAT SCI COUNCIL.

XX Wu H, Shr G;  
XX  
XX WPI; 2001-326604/34.  
XX N-PSDB; AAF82144.  
XX

XX Preparation of novel streptokinase mutants as improved thrombolytic  
agents -  
XX  
XX Claim 1; Page 1; 4pp; Chinese.

XX The present invention describes a method to create mutants of  
streptokinase (SK) which become more resistant to hydrolytic  
inactivation by human plasmin (HPlm) and more effective in activation  
of human plasminogen (HPIg) than the native SK that is commercially  
available. The novel HPlm hydrolysis resistant SK can be created by the  
techniques of gene engineering to substitute the amino acid residues  
near the peptide bonds that are hydrolysed by HPlm. The mutant SK can  
be used to form HPIg and native SK and could be used as a thrombolytic  
agent. The mutant SK sequence could be coupled with other proteins to  
form fusion proteins and improve the fibrinolytic activity of the  
fusion proteins. Some truncated SKs such as SK(16-378) could activate  
HPIg as efficiently as native SK. The truncated SKs comprising the  
modification of Pro58-Lys59-Ser60-Lys61 to other amino acids would have  
a better thrombolytic activity than the corresponding native truncated  
SK. Since Lys59-Ser60 is among the few peptide bonds which are cleaved  
in the early reaction with HPlm and the NH<sub>2</sub>-terminal peptide chain of  
SK, Lys59 is essential in stabilising the structure of SK, the mutation  
at/or near by the peptide bond of Lys59-Ser60 should be able to prevent  
the hydrolysis of the peptide bond and might improve the stability of  
SK as a HPIg activator. The present sequence represents the mutant  
streptokinase (K59E) given in the present invention.  
XX N.B. The present sequence corresponds to the indexers best interpretation  
of the sequence given in the specification, which is of poor quality  
print.

XX Sequence 414 AA;  
SQ Query Match 100.0%; Score 30; DB 22; Length 414;  
Best Local Similarity 100.0%; Pred. No. 76;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVEY 6  
Db 157 SVDVEY 162

RESULT 43  
AAAY9593  
ID AAAY9593 standard; protein; 415 AA.  
XX  
AC AAAY9593;  
XX  
XX 13-SEP-2000 (first entry)  
XX  
DE Streptococcus plasminogen activator, streptokinase.  
XX  
KW Plasminogen activator; cardiant; thrombolytic;  
KW heart attack; stroke; blood clotting disorder.  
XX  
OS Streptococcus sp.  
XX  
XX WO2000032759-A1.  
XX  
XX 08-JUN-2000.  
XX  
XX 06-MAY-1999; 99WO-US09991.  
XX  
XX 02-DEC-1998; 98US-0110588.  
XX  
XX (OKLA-) OKLAHOMA MEDICAL RES FOUND.  
XX  
XX Lin X, Zhang XC, Tang JUN;  
XX  
XX WPI; 2000-422975/36.  
XX  
XX Polypeptide with plasminogen activator activity useful as thrombolytic  
agent for treating blood clot disorders e.g. heart attack, comprises 10  
amino acid peptide fragment for recognition or activation of  
plasminogen -  
XX  
XX Disclosure; Page 29-31; 41pp; English.  
XX  
XX The present sequence is streptokinase, a single-peptide secretory  
protein which is produced by various strains of haemolytic Streptococcus.  
Streptokinase forms a tight binding complex with human plasminogen,  
causing the spontaneous conversion of plasminogen to its active form,  
plasmin. Plasminogen is the principal serine protease zymogen in the  
extracellular fluids of vertebrates. Plasmin is implicated in  
pericellular proteolysis associated with a wide range of physiological  
and pathological processes. Plasminogen activators regulate plasminogen  
expression either by forming a binding complex, as in the case of  
streptokinase, or by hydrolysing a peptide bond in plasminogen to convert  
it to plasmin. Review of sequence homologies of several plasminogen  
activators and chymotrypsin has identified a six amino acid peptide  
involved in plasminogen activation. This peptide is particularly useful  
when inserted between amino acid residues 644 and 645 of full length  
human plasminogen. Novel plasminogen activators have been made based upon  
the plasminogen activation/recognition site of plasminogen binding  
proteins. The polypeptides are useful in preparing thrombolytic agents  
for treating blood clotting disorders such as heart attack.  
XX  
XX Sequence 415 AA;  
SQ Query Match 100.0%; Score 30; DB 21; Length 415;  
Best Local Similarity 100.0%; Pred. No. 77;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVEY 6  
Db 157 SVDVEY 162

RESULT 44  
AAAY50870  
ID AAAY50870 standard; protein; 415 AA.  
XX  
XX AAAY50870;  
AC  
XX

DT 24-FEB-2000 (first entry)  
 XX Streptococcus sp. streptokinase protein fragment.  
 DE Thrombolytic agent; streptokinase; antigenic; blood clot; heart attack;  
 XX treatment.  
 KW Homo sapiens.  
 XX WO9957251-A2.  
 XX 11-NOV-1999.  
 XX 06-MAY-1999; 99WO-US10086.  
 XX 06-MAY-1998; 98US-0084392.  
 XX (OKLA-) OKLAHOMA MEDICAL RES FOUND.  
 XX Zhang XC, Lin X, Tang JUN;  
 XX WPI; 2000-052966/04.  
 XX New thrombolytic agents derived from modified humanized streptokinase,  
 PT useful for treating blood clot disorders -  
 XX Example 5; Page 48-49; 55pp; English.  
 XX This invention describes a novel thrombolytic agent comprising  
 CC streptokinase where at least one nonessential portion has been modified.  
 CC The invention also describes a method of forming a thrombolytic agent  
 CC comprising determining a nonessential portion of streptokinase and  
 CC modifying the nonessential portion to render the resulting protein less  
 CC antigenic. The modified streptokinase is used to treat blood clot  
 CC disorders, such as heart attacks. The modified streptokinase has less  
 CC antigenicity than streptokinase but is still able to complex plasminogen  
 CC and lead to plasminogen activation. Modified streptokinase with the  
 CC nonessential portions removed or truncated simplify the molecule. Such  
 CC smaller proteins are cheaper and easier to produce. This sequence  
 CC represents a fragment of a Streptococcus sp. streptokinase protein  
 CC which is used in the description of the method of the invention.  
 XX  
 SQ Sequence 415 AA;  
 Query Match 100.0%; Score 30; DB 21; Length 415;  
 Best Local Similarity 100.0%; Pred. No. 77;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SVDVEY 6  
 DB 157 SVDVEY 162  
 RESULT 45  
 AAP50620  
 ID AAP50620 standard; Protein; 440 AA.  
 XX AAP50620;  
 XX 16-OCT-1991 (first entry)  
 DE Sequence encoded by skc streptokinase gene on the 2.5kb PetI  
 DE produced pMFI fragment.  
 XX Enzyme; thrombolytic agent; blood clot.  
 XX Streptococcus equisimilis strain H46A (serological group C).  
 XX AU8433859-A.  
 XX 18-APR-1985.  
 XX 05-OCT-1984; 84AU-0033859.

XX 02-MAR-1984; 84US-0585417.  
 PR 10-OCT-1983; 83DD-0255523.  
 PR 10-OCT-1983; 83DD-0255235.  
 XX (PHIP ) PHILLIPS PETROLEUM CO.  
 PA (UYOK-) UNIV OF OKLAHOMA.  
 XX Ferretti JJ, Malke H;  
 XX WPI; 1985-135032/23.  
 DR N-PSDB; AAN50493.  
 XX Streptokinase prodn. - by cultivating Escherichia coli ATCC 39613  
 PT contg. recombinant plasmid pMFI  
 XX Example; Fig 2; 28pp; English.  
 CC Streptokinase produced using E.coli transformed with a recombinant  
 CC streptokinase vector can be isolated for use as a thrombolytic agent  
 CC to facilitate the in vivo lysis or dissolution of blood clots. The  
 CC vector is esp. a plasmid obtd. from E.coli, esp. plasmid pBR 322.  
 CC Recombinant plasmid pMFI as defined by a restriction endonuclease  
 CC map is claimed. Escherichia coli HB 101 harbouring plasmid pMFI is  
 CC deposited as ATCC 39613.  
 XX  
 SQ Sequence 440 AA;  
 Query Match 100.0%; Score 30; DB 6; Length 440;  
 Best Local Similarity 100.0%; Pred. No. 82;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SVDVEY 6  
 DB 183 SVDVEY 188  
 RESULT 46  
 AAR06378  
 ID AAR06378 standard; protein; 440 AA.  
 XX AAR06378;  
 XX 25-MAR-2003 (updated)  
 DT 20-DEC-1990 (first entry)  
 XX Streptokinase A from Streptococcus pyogenes SFI30/13.  
 DE Streptokinase A; recombinant phase; thrombolytic agent; plasminogen;  
 KW plasmid.  
 XX Streptococcus pyogenes.  
 XX DD276694-A.  
 PN 07-MAR-1990.  
 PD 07-NOV-1988; 88DD-0321532.  
 PF 07-NOV-1988; 88DD-0321532.  
 PR 07-NOV-1988; 88DD-0321532.  
 XX (DEAK ) AKAD WISSENSCHAFTEN DDR.  
 PA Walter F, Siegel M, Malke H;  
 XX WPI; 1990-247328/33.  
 DR N-PSDB; AAQ05604.  
 XX High yield streptokinase A prodn. from infected bacteria - contg.  
 PT recombinant phase including gene from Streptococcus, useful as  
 PT thrombolytic agent  
 XX Disclosure; Fig 2; 7pp; German.

XX Lambda L47.1 is ligated with genomic DNA from S. pyogenes SPI30/13  
CC and the resultant product used to transform bacteria. Infected  
CC cells are cultured in liq. medium contg. assimilable C and N sources,  
CC and streptokinase A is isolated from the cell lysate.  
CC The infected cells provide the protein in high yields, i.e.  
CC 1000 U/ml compared to 80 U/ml for the donor strain.  
CC The protein activates the autocatalytic conversion of human  
CC plasminogen to human plasmin, so is potentially useful as a thrombolytic  
CC agent. See also DD-276693 (AAQ05603).  
CC (Updated on 25-MAR-2003 to correct PA field.)  
XX  
SQ Sequence 440 AA;  
  
Query Match 100.0%; Score 30; DB 11; Length 440;  
Best Local Similarity 100.0%; Pred. No. 82;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 SVDVEY 6  
Db 183 SVDVEY 188  
|||||  
  
RESULT 47  
AAR06377  
ID AAR06377 standard; protein; 440 AA.  
XX  
AC AAR06377;  
XX  
DT 25-MAR-2003 (updated)  
DT 20-DEC-1990 (first entry)  
XX  
DE Streptokinase G protein from Streptococcus pyogenes G19908.  
XX  
KW Streptokinase G; thrombolytic agent; plasminogen; plasmin;  
KW recombinant plasmid.  
XX  
OS Streptococcus pyogenes.  
XX  
PN DD276693-A.  
XX  
PD 07-MAR-1990.  
XX  
PF 07-NOV-1988; 88DD-0321531.  
XX  
PR 07-NOV-1988; 88DD-0321531.  
XX  
PA (DEAK ) AKAD WISSENSCHAFTEN DDR.  
XX  
PI Walter F, Siegel M, Malke H;  
XX  
PS WPI; 1990-247327/33.  
XX  
DR N-PSDB; AAQ05603.  
XX  
PT High yield streptokinase G prodn. from recombinant cells -  
PT transformed with plasmid contg. gene from Streptococcus, useful  
PT as thrombolytic agent  
XX  
PS Disclosure; Fig 2; 7pp; German.  
XX  
CC Plasmid pMW1 ( contg. the streptokinase G gene ) is ligated with  
CC pUC19 and the resultant product used to transform bacteria. Infected  
CC cells are cultured in liq. medium contg. assimilable C and N sources,  
CC and streptokinase G is isolated from the cell lysate.  
CC The infected cells provide the protein in high yields, i.e.  
CC 600 U/ml which is 1.5-2 times that for the donor strain.  
CC The protein activates the autocatalytic conversion of human  
CC plasminogen to human plasmin, so is potentially useful as a thrombolytic  
CC agent. See also DD-276694 (AAQ05604).  
CC (Updated on 25-MAR-2003 to correct PA field.)  
XX  
SQ Sequence 440 AA;

Query Match 100.0%; Score 30; DB 11; Length 440;  
Best Local Similarity 100.0%; Pred. No. 82;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 SVDVEY 6  
Db 183 SVDVEY 188  
|||||  
  
RESULT 48  
AAR12889  
ID AAR12889 standard; Protein; 440 AA.  
XX  
AC AAR12889;  
XX  
DT 25-MAR-2003 (updated)  
DT 17-SEP-1991 (first entry)  
XX  
DE Streptokinase.  
XX  
KW Fusion protein; blood clotting; coagulation; fibrinolysis;  
KW antithrombotic; thrombolysis; streptokinase.  
XX  
OS Streptococcus equisimilis ATCC 9542 or ATCC 100009.  
XX  
FH Key Location/Qualifiers  
FT Peptide 1..26  
FT /label= signal sequence  
FT Protein 27..440  
FT /label= mature streptokinase  
XX  
PN WO9109125-A.  
XX  
PD 27-JUN-1991.  
XX  
PF 07-DEC-1990; 90WO-GB01911.  
XX  
PR 07-DEC-1990; 90WO-GB01911.  
PR 07-DEC-1989; 89GB-0027722.  
XX  
PA (BRBI-) BRITISH BIO-TECHNOLOGY LTD.  
XX  
PI Dawson KM, Hunter MG, Czaplewski LG;  
XX  
XX WPI; 1991-208151/28.  
DR N-PSDB; AAQ12156.  
XX  
PT Fusion protein cleavage by blood clotting enzyme - for prodn. of  
PT fractions having greater antithrombotic activity for therapy and  
PT prophylaxis.  
XX  
PS Disclosure; Page 80; 115pp; English.  
XX  
CC The sequence was deduced from PCR amplified chromosomal DNA from  
CC S. equisimilis (Lancefield's Gp C ) ATCC 10009 or ATCC 9642. The  
CC primers used for the PCR were based on the published DNA sequence  
CC of S. equisimilis strain H46A (Malke, H., Roe, B., and Ferretti,  
CC J.J., Gene 34 357-362 [1985]). See Swiss-Prot K02986 and P00779  
CC and Geneseg N70106. The gene can be used to construct expression  
CC vectors in which the streptokinase gene is linked to a second gene  
CC encoding e.g. another streptokinase protein, hirudin, or a strepto-  
CC kinase-like protein, via a linking sequence encoding a cleavage  
CC site for e.g. factor Xa or thrombin. The enzymes which cleave the  
CC fusion protein are present at the site of the target thrombus so  
CC the active agents are released specifically at the place where clot  
CC formation is occurring.  
CC See also R12887, R12888, R12891-R12894, R12885 and R12522.  
CC (Updated on 25-MAR-2003 to correct PA field.)  
XX  
SQ Sequence 440 AA;  
  
Query Match 100.0%; Score 30; DB 12; Length 440;  
Best Local Similarity 100.0%; Pred. No. 82;



Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVEY 6  
Db 183 SVDVEY 188  
RESULT 49  
ABP29561  
ID ABP29561 standard; Protein; 440 AA.  
XX  
AC ABP29561;  
XX  
DT 02-JUL-2002 (first entry)  
XX  
DE Streptococcus polypeptide SEQ ID NO 8298.  
XX  
KW Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae;  
KW group A streptococcus; Streptococcus pyogenes; antibacterial;  
KW antiinflammatory; infection; vaccine; meningitis; gene therapy.  
XX  
OS Streptococcus pyogenes.  
XX  
PN WO200234771-A2.  
XX  
PD 02-MAY-2002.  
XX  
PF 29-OCT-2001; 2001WO-GB04789.  
XX  
PR 27-OCT-2000; 2000GB-0026333.  
PR 24-NOV-2000; 2000GB-0028727.  
PR 07-MAR-2001; 2001GB-0005640.  
XX  
PA (CHIR-) CHIRON SPA.  
PA (GENO-) INST GENOMIC RES.  
XX  
PI Telford J, Masignani V, Margarit Ros YI, Grandi G, Fraser C;  
PI Tettelin H;  
XX  
DR WPI; 2002-352536/38.  
DR N-PSDB; ABN70192.  
XX  
XX New Streptococcus protein for the treatment or prevention of infection  
PT or disease caused by Streptococcus bacteria, such as meningitis, and  
PT for detecting a compound that binds to the protein.  
XX  
PS Claim 1; Page 3946; 4525pp; English.  
XX  
CC The invention relates to a protein (ABP25413-ABP30895) from group B  
CC streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS  
CC (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in  
CC the specification. The proteins have antibacterial and antiinflammatory  
CC activity. (I), nucleic acids encoding (I), ABN66044-ABN71526 and  
CC antibodies that bind (I) are used in the manufacture of medicaments for  
CC the treatment or prevention of infection or disease caused by  
CC Streptococcus bacteria, particularly S. agalactiae and S. pyogenes.  
CC Nucleic acids encoding (I) are used to detect Streptococcus in a  
CC biological sample. (I) is used to determine whether a compound binds to  
CC (I). A composition comprising (I) or a nucleic acid encoding (I), may be  
CC used as a vaccine or diagnostic composition. The disease caused by  
CC Streptococcus that is prevented or treated may be meningitis. Nucleic  
CC acid encoding (I) may be used to recombinantly produce (I) and may be  
CC used in gene therapy. Antibodies to (I) are used for affinity  
CC chromatography, immunoassays, and distinguishing/identifying  
CC Streptococcus proteins.  
XX  
SQ Sequence 440 AA;

Query Match 100.0%; Score 30; DB 23; Length 440;  
Best Local Similarity 100.0%; Pred. No. 82;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SVDVEY 6

Db 183 SVDVEY 188  
RESULT 50  
AAR12885  
ID AAR12885 standard; Protein; 483 AA.  
XX  
AC AAR12885;  
XX  
DT 25-MAR-2003 (updated)  
DT 17-SEP-1991 (first entry)  
XX  
DB Factor Xa-cleavable hirudin-IEGR-streptokinase.  
XX  
KW Fusion protein; blood clotting; coagulation; fibrinolysis;  
KW antithrombotic; thrombolysis.  
XX  
OS Synthetic.  
FH Key Location/Qualifiers  
FT Protein 1..65  
FT Peptide /label= hirudin HV-1  
FT Peptide 66..69  
FT /label= linker  
FT /note= "factor Xa cleavage site"  
FT Protein 70..483  
FT /label= streptokinase  
XX  
PN WO9109125-A.  
XX  
PD 27-JUN-1991.  
XX  
PF 07-DEC-1990; 90WO-GB01911.  
XX  
PR 07-DEC-1990; 90WO-GB01911.  
PR 07-DEC-1989; 89GB-0027722.  
XX  
PA (BRBI-) BRITISH BIO-TECHNOLOGY LTD.  
XX  
PI Dawson KM, Hunter MG, Czaplewski LG;  
XX  
DR WPI; 1991-208151/28.  
DR N-PSDB; AAQ12162.  
XX  
PT Fusion protein cleavage by blood clotting enzyme - for prodn. of  
PT fractions having greater antithrombotic activity for therapy and  
PT prophylaxis.  
XX  
PS Disclosure; Page 96; 115pp; English.  
XX  
CC The protein is a recombinant product of a gene fusion construct.  
CC The sequence of the synthetic hirudin HV-1 genes was designed  
CC based on the published amino acid sequence (Dodd J., et al FEBS  
CC Letters 165 180 (1984)). The sequence of streptokinase was obtd.  
CC from PCR amplified chromosomal DNA from S. equisimilis ATCC 10009  
CC or ATCC 9642. The primers used for the PCR were based on the pub-  
CC lished DNA sequence of S. equisimilis strain H46A (Malke, H., Roe,  
CC B., and Ferretti, J.J., Gene 34 357-362 [1985]). The two  
CC sequences were used to construct an expression vector in which the  
CC hirudin gene is linked to the streptokinase gene via a linking  
CC sequence encoding a cleavage site for factor Xa. The factor Xa is  
CC present at the site of the target thrombus so the active agents are  
CC released specifically at the place where clot formation is occurring.  
CC See also AAR12887-R12889, AAR12891-R12894 and AAR12522.  
XX  
SQ Sequence 483 AA;

Query Match 100.0%; Score 30; DB 12; Length 483;  
Best Local Similarity 100.0%; Pred. No. 91;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SVDVEY 6

QY 1 SVDVEY 6  
Db 226 SVDVEY 231

RESULT 51  
AAR12522  
ID AAR12522 standard; Protein; 483 AA.  
XX AAR12522;  
XX 25-MAR-2003 (updated)  
DT 17-SEP-1991 (first entry)  
XX Factor Xa-cleavable streptokinase-LEGR-hirudin.  
XX Fusion protein; blood clotting; coagulation; fibrinolysis;  
KW antithrombotic; thrombolysis.  
XX Synthetic.  
XX Key Location/Qualifiers  
FH Protein 1..414  
FT Peptide /label= streptokinase  
FT Peptide 415..418  
FT /label= linker  
FT /note= "factor Xa cleavage site"  
FT 419..483  
FT /label= hirudin  
XX WO9109125-A.  
XX 27-JUN-1991.  
XX 07-DEC-1990; 90WO-GB01911.  
XX 07-DEC-1990; 90WO-GB01911.  
PR 07-DEC-1989; 89GB-0027722.  
XX (BRBI-) BRITISH BIO-TECHNOLOGY LTD.  
XX Dawson KM, Hunter MG, Czaplewski LG;  
XX WPI; 1991-208151/28.  
DR N-PSDB; AAQ12490.  
XX Fusion protein cleavage by blood clotting enzyme - for prodn. of  
PT fractions having greater antithrombotic activity for therapy and  
PT prophylaxis.  
XX Disclosure; Page 96; 115pp; English.  
XX The protein is a recombinant product of a gene fusion construct.  
CC The sequence of the synthetic hirudin HV-1 genes was designed  
CC based on the published amino acid sequence (Dodd J., et al FEBS  
CC Letters 165 180 (1984)). The sequence of streptokinase was obtd.  
CC from PCR amplified chromosomal DNA from S. equisimilis ATCC 10009  
CC or ATCC 9642. The primers used for the PCR were based on the pub-  
CC lished DNA sequence of S. equisimilis strain H46A (Malke, H., Roe,  
CC B., and Ferretti, J.J., Gene 34 357-362 [1985]). The two  
CC sequences were used to construct an expression vector in which the  
CC streptokinase gene is linked to the hirudin gene via a linking  
CC sequence encoding a cleavage site for factor Xa. The factor Xa is  
CC present at the site of the target thrombus so the active agents are  
CC released specifically at the place where clot formation is occurring.  
CC See also AAR12887-R12889, AAR12891-R12894 and AAR12885.  
CC (Updated on 25-MAR-2003 to correct PA field.)  
XX SQ Sequence 483 AA;  
Query Match 100.0%; Score 30; DB 12; Length 483;  
Best Local Similarity 100.0%; Pred. No. 91;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVEY 6  
Db 157 SVDVEY 162

RESULT 52  
AAR12891  
ID AAR12891 standard; Protein; 499 AA.  
XX AAR12891;  
XX 25-MAR-2003 (updated)  
DT 17-SEP-1991 (first entry)  
XX Streptokinase fused to yeast alpha factor secretion sequence.  
XX Fusion protein; blood clotting; coagulation; fibrinolysis;  
KW antithrombotic; thrombolysis; streptokinase.  
XX Streptococcus equisimilis ATCC 9542 or ATCC 100009.  
XX Key Location/Qualifiers  
FH Peptide 1..85  
FT /label= pre-pro alpha factor secretion sequence  
FT /note= "S. cerevisiae"  
FT Protein 86..499  
FT /label= mature streptokinase  
XX WO9109125-A.  
XX 27-JUN-1991.  
XX 07-DEC-1990; 90WO-GB01911.  
XX 07-DEC-1990; 90WO-GB01911.  
PR 07-DEC-1989; 89GB-0027722.  
XX (BRBI-) BRITISH BIO-TECHNOLOGY LTD.  
XX Dawson KM, Hunter MG, Czaplewski LG;  
XX WPI; 1991-208151/28.  
DR N-PSDB; AAQ12158.  
XX Fusion protein cleavage by blood clotting enzyme - for prodn. of  
PT fractions having greater antithrombotic activity for therapy and  
PT prophylaxis.  
XX Disclosure; Page 86; 115pp; English.  
XX The streptokinase sequence was obtd. from PCR amplified chromosomal  
CC DNA from S. equisimilis (Lancefield's Gp C) ATCC 10009 or ATCC 9642  
CC (the primers used for the PCR were based on the published DNA  
CC sequence of S. equisimilis strain H46A (Malke, H., Roe, B., and  
CC Ferretti, J.J., Gene 34 357-362 [1985])). The gene was fused to  
CC DNA encoding the yeast alpha factor pre-pro-secretion sequence in  
CC an expression vector, pSMD1/152, for prodn. of recombinant strepto-  
CC kinase in S. cerevisiae strain BJ2168.  
CC See also AAR12887-R12889, AAR12892-R12894, AAR12885 and AAR12522.  
CC (Updated on 25-MAR-2003 to correct PA field.)  
XX SQ Sequence 499 AA;  
Query Match 100.0%; Score 30; DB 12; Length 499;  
Best Local Similarity 100.0%; Pred. No. 94;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 53  
 AAR11829  
 ID AAR11829 standard; Protein; 531 AA.  
 XX  
 AC AAR11829;  
 XX  
 DT 08-JUL-1991 (first entry)  
 XX  
 DE FB-FB-SK fusion conjugate.  
 XX  
 XX Fibrin-binding protein; fibrinolysis; intravascular thrombi;  
 KW fibrinogen; streptokinase; fusion protein.  
 XX  
 OS Staphylococcus aureus.  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 2..61  
 FT /label= FB monomer  
 FT Peptide 62..119  
 FT /label= FB monomer  
 FT Peptide 120..531  
 FT /label= streptokinase  
 XX  
 PN US5011686-A.  
 XX  
 PD 30-APR-1991.  
 XX  
 PF 15-NOV-1989; 89US-0437769.  
 XX  
 PR 21-SEP-1987; 87US-0099242.  
 PR 15-NOV-1989; 89US-0437769.  
 XX  
 PA (CREA-) CREATIVE BIOMOLEC.  
 XX  
 PI Pang RHU;  
 XX  
 DR WPI; 1991-140198/19.  
 DR N-PSDB; AAQ11651.  
 XX  
 XX Imparting injectable fibrinolytic agent - with affinity for  
 PT intravascular thrombus, by linking agent to fibrin binding domain.  
 PS Disclosure; Fig 5; 18pp; English.  
 XX  
 XX The conjugate comprises an FB-FB dimer linked to streptokinase  
 CC The FB fragment has selective affinity for fibrin, low affinity  
 CC for fibrinogen, and minimal immunogenicity, imparting thrombus-  
 CC targeting capability.  
 CC See also AAR11821 and AAR11828.  
 XX  
 SQ Sequence 531 AA;  
 Query Match 100.0%; Score 30; DB 12; Length 531;  
 Best Local Similarity 100.0%; Pred. No. 1e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SVDVEY 6  
 DB 274 SVDVEY 279  
 |||||  
 RESULT 54  
 AAY24798  
 ID AAY24798 standard; Protein; 736 AA.  
 XX  
 AC AAY24798;  
 XX  
 DT 26-AUG-1999 (first entry)  
 XX  
 DE Recombinant streptokinase rSK60-414.  
 XX  
 XX Streptococcus; streptokinase; fibrin-dependent plasminogen activator;  
 KW rSK; rSK; bacterial; blood clot; thrombotic condition;

KW myocardial infarction; venous thrombosis; pulmonary embolism;  
 KW cerebral thrombosis; graft thrombosis; arterial thrombosis.  
 XX  
 OS Streptococcus equisimilis.  
 OS Synthetic.  
 XX  
 PN WO9931247-A1.  
 XX  
 PD 24-JUN-1999.  
 XX  
 PF 15-DEC-1998; 98WO-US26694.  
 XX  
 PR 15-DEC-1997; 97US-0069497.  
 XX  
 PA (HARD ) HARVARD COLLEGE.  
 XX  
 PI Reed GL;  
 XX  
 DR WPI; 1999-395183/33.  
 DR N-PSDB; AAX83589.  
 XX  
 PT N-terminally deleted streptokinase  
 XX  
 PS Disclosure; Page 55-58; 73pp; English.  
 XX  
 CC The present invention describes an isolated bacterial protein that  
 CC induces fibrin-dependent plasminogen activation in a pharmaceutical  
 CC composition for dissolving blood clots. Also described are: (1) a  
 CC composition comprising an isolated modified streptokinase, the  
 CC modification being removal of amino acid residues in the amino terminus;  
 CC (2) a method for dissolving a blood clot in a subject, comprising  
 CC administering to the subject a fibrin-dependent streptokinase protein;  
 CC a nucleic acid (I) encoding a modified bacterial streptokinase; (3) an  
 CC expression vector comprising (I); and (4) a host cell transformed with  
 CC the expression vector of (3). The pharmaceutical composition comprising  
 CC a bacterial fibrin-dependent plasminogen activator is useful for  
 CC dissolving blood clots in patients with a thrombotic condition, e.g.  
 CC myocardial infarction, venous thrombosis, pulmonary embolism, cerebral  
 CC thrombosis, graft thrombosis and arterial thrombosis. The modified  
 CC streptokinase can also be used in non-human mammals. Streptokinase  
 CC activation of plasminogen is at least 10-fold, preferably 100-fold  
 CC greater in the presence of fibrin than in the absence of fibrin. The  
 CC modified streptokinase has at least one amino acid substitution that  
 CC inactivates a substrate site for proteolytic cleavage. This reduces the  
 CC rate of degradation of the streptokinase at least two-fold. The present  
 CC sequence represents recombinant streptokinase, designated rSK60-414.  
 XX  
 SQ Sequence 736 AA;  
 Query Match 100.0%; Score 30; DB 20; Length 736;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SVDVEY 6  
 DB 479 SVDVEY 484  
 |||||  
 RESULT 55  
 AAR12894  
 ID AAR12894 standard; Protein; 747 AA.  
 XX  
 AC AAR12894;  
 XX  
 DT 25-MAR-2003 (updated)  
 DT 17-SEP-1991 (first entry)  
 XX  
 DE Met-core streptokinase-core streptokinase.  
 XX  
 KW Fusion protein; blood clotting; coagulation; fibrinolysis;  
 KW antithrombotic; thrombolysis; streptokinase; thrombin.  
 XX  
 OS Streptococcus equisimilis ATCC 9542 or ATCC 100009.

XX Key Location/Qualifiers  
FH 2..369  
FT /label= core streptokinase  
FT /note= "AAs 16-383"  
FT 370..379  
FT /label= thrombin cleavage site  
FT 380..747  
FT /label= core streptokinase  
FT /note= "AAs 16-383"  
XX  
PN W09109125-A.  
XX  
XX 27-JUN-1991.  
XX  
XX 07-DEC-1990; 90WO-GB01911.  
XX  
XX 07-DEC-1990; 90WO-GB01911.  
PR 07-DEC-1989; 89GB-0027722.  
XX  
XX (BRBI-) BRITISH BIO-TECHNOLOGY LTD.  
XX  
XX Dawson KM, Hunter MG, Czaplowski LG;  
XX  
XX WPI; 1991-208151/28.  
DR N-PSDB; AAQ12161.  
XX  
XX Fusion protein cleavage by blood clotting enzyme - for prodn. of  
PT fractions having greater antithrombotic activity for therapy and  
PT prophylaxis.  
XX  
XX Disclosure; Page 93; 115pp; English.  
XX  
XX The sequence was deduced from DNA obtd. from PCR amplified chromo-  
CC somal DNA from S. equisimilis (lanecfield's Gp C ) ATCC 10009 or  
CC ATCC 9642. The gene was tuncated by 15 codons at the 3' terminal  
CC and one copy engineered to add a Met codon prior to codon 16 of the  
CC CDS. The two truncated genes were used to construct an expression  
CC vector in which they were linked via a sequence encoding a cleavage  
CC site for thrombin which, when cleaved, releases the individual pro-  
CC teins which have antithrombotic activity. The thrombin is present  
CC at the site of the target thrombus so the active agents are released  
CC specifically at the place where clot formation is occurring.  
CC See also AAR12887-R12889, AAR12891-R12893, AAR12885 and AAR12522.  
CC (Updated on 25-MAR-2003 to correct PA field.)  
XX  
XX Sequence 747 AA;  
SQ  
Query Match 100.0%; Score 30; DB 12; Length 747;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SVDVEY 6  
Db 143 SVDVEY 148  
RESULT 56  
RAY24797  
ID AAY24797 standard; Protein; 795 AA.  
XX  
XX AAY24797;  
AC  
XX 26-AUG-1999 (first entry)  
DT  
XX Streptokinase and maltose binding protein fusion protein.  
DE  
XX Streptococcus; streptokinase; fibrin-dependent plasminogen activator;  
XX nSK; xSK; bacterial; blood clot; thrombotic condition;  
XX myocardial infarction; venous thrombosis; pulmonary embolism;  
XX cerebral thrombosis; graft thrombosis; arterial thrombosis.  
XX  
XX Streptococcus equisimilis.  
OS

OS Synthetic.  
XX W09931247-A1.  
PN  
XX 24-JUN-1999.  
PD  
XX 15-DEC-1998; 98WO-US26694.  
XX  
XX 15-DEC-1997; 97US-0069497.  
PR  
XX (HARD ) HARVARD COLLEGE.  
PA  
XX Reed GL;  
XX  
XX WPI; 1999-395183/33.  
DR N-PSDB; AAX80497.  
Lk  
XX N-terminally deleted streptokinase  
PT  
XX Example; Page 48-51; 73pp; English.  
PS  
XX The present invention describes an isolated bacterial protein that  
CC induces fibrin-dependent plasminogen activation in a pharmaceutical  
CC composition for dissolving blood clots. Also described are: (1) a  
CC composition comprising an isolated modified streptokinase, the  
CC modification being removal of amino acid residues in the amino terminus;  
CC (2) a method for dissolving a blood clot in a subject, comprising  
CC administering to the subject a fibrin-dependent streptokinase protein;  
CC a nucleic acid (1) encoding a modified bacterial streptokinase; (3) an  
CC expression vector comprising (1); and (4) a host cell transformed with  
CC the expression vector of (3). The pharmaceutical composition comprising  
CC a bacterial fibrin-dependent plasminogen activator is useful for  
CC dissolving blood clots in patients with a thrombotic condition, e.g.  
CC myocardial infarction, venous thrombosis, pulmonary embolism, cerebral  
CC thrombosis, graft thrombosis and arterial thrombosis. The modified  
CC streptokinase can also be used in non-human mammals. Streptokinase  
CC activation of plasminogen is at least 10-fold, preferably 100-fold  
CC greater in the presence of fibrin than in the absence of fibrin. The  
CC modified streptokinase has at least one amino acid substitution that  
CC inactivates a substrate site for proteolytic cleavage. This reduces the  
CC rate of degradation of the streptokinase at least two-fold. The present  
CC sequence represents a streptokinase and maltose binding protein fusion  
CC protein from an example of the present invention.  
XX  
XX Sequence 795 AA;  
SQ  
Query Match 100.0%; Score 30; DB 20; Length 795;  
Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SVDVEY 6  
Db 538 SVDVEY 543  
RESULT 57  
AAW21723  
ID AAW21723 standard; Protein; 800 AA.  
XX  
XX AAW21723;  
AC  
XX 01-OCT-1997 (first entry)  
DT  
XX Plasminogen-binding domain from streptokinase.  
DE  
XX Plasminogen-binding fragment; streptokinase; degradation;  
XX thrombolytic agent; blood clot; bolus.  
KW  
XX Streptococcus equisimilis.  
OS  
XX W09641883-A1.  
PN  
XX 27-DEC-1996.  
PD

XX PF 07-JUN-1996; 96WO-US09640.  
XX PR 09-JUN-1995; 95US-0488940.  
XX PA (HARD ) HARVARD COLLEGE.  
XX PI Reed GL;  
XX PI WPI; 1997-065469/06.  
XX PT Modified forms of streptokinase resistant to enzymatic cleavage -  
XX PT useful as thrombolytic agents in treating thrombosis and in medical  
XX PT equipment  
XX PS Claim 2; Page 35-37; 65pp; English.  
XX CC This sequence represents the plasminogen-binding fragment of  
XX CC streptokinase which lacks the N-terminal 14 amino acids. This  
XX CC modified streptokinase has an in vitro degradation rate at least  
XX CC 2 times slower than that of native streptokinase. Compounds  
XX CC containing modified streptokinases are specifically used as  
XX CC thrombolytic agents for dissolving blood clots in vivo in a  
XX CC mammal, preferably at a dose of 20000 U/kg, opt. as a bolus  
XX CC rather than by continuous infusion.  
XX CC  
XX SQ Sequence 800 AA;  
Query Match 100.0%; Score 30; DB 18; Length 800;  
Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SVDVEY 6  
DB 143 SVDVEY 148  
RESULT 58  
AAW21728  
ID AAW21728 standard; protein; 813 AA.  
XX AC AAW21728;  
XX DT 01-OCT-1997 (first entry)  
XX DE Wild type plasminogen-binding fragment of Streptokinase.  
XX KW Plasminogen-binding fragment; streptokinase; degradation; MBP;  
XX KW thrombolytic agent; blood clot; bolus; maltose-binding protein.  
XX OS Streptococcus equisimilis.  
XX PN WO9641883-A1.  
XX PD 27-DEC-1996.  
XX PF 07-JUN-1996; 96WO-US09640.  
XX PR 09-JUN-1995; 95US-0488940.  
XX PA (HARD ) HARVARD COLLEGE.  
XX PI Reed GL;  
XX PI WPI; 1997-065469/06.  
XX PT Modified forms of streptokinase resistant to enzymatic cleavage -  
XX PT useful as thrombolytic agents in treating thrombosis and in medical  
XX PT equipment  
XX PS Example 1; Page 12-13; 65pp; English.  
XX CC This sequence represents the wild type plasminogen-binding fragment

XX of streptokinase. This fragment was used in the design of a  
XX modified streptokinase has an in vitro degradation rate at least  
XX 2 times slower than that of native streptokinase. Compounds  
XX containing modified streptokinases are specifically used as  
XX thrombolytic agents for dissolving blood clots in vivo in a  
XX mammal, preferably at a dose of 20000 U/kg, opt. as a bolus  
XX rather than by continuous infusion.  
XX SQ Sequence 813 AA;  
Query Match 100.0%; Score 30; DB 18; Length 813;  
Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SVDVEY 6  
DB 156 SVDVEY 161  
RESULT 59  
AAR12893  
ID AAR12893 standard; protein; 859 AA.  
XX AC AAR12893;  
XX DT 25-MAR-2003 (updated)  
XX DT 17-SEP-1991 (first entry)  
XX DE OmpAL streptokinase-streptokinase gene.  
XX KW Fusion protein; blood clotting; coagulation; fibrinolysis;  
XX KW antithrombotic; thrombolysis; major outer membrane protein A;  
XX KW thrombin; ss.  
XX OS Streptococcus equisimilis ATCC 9542 or ATCC 100009.  
XX FH Key Location/Qualifiers  
XX FT Peptide 1..21  
FT /label= OmpAL signal sequence  
FT /note= "from E. Coli"  
FT Protein 22...435  
FT /label= streptokinase  
FT Cleavage-site 436..445  
FT /label= linking peptide  
FT /note= "cleavage site for thrombin"  
FT Protein 446..859  
FT /label= streptokinase  
XX PN WO9109125-A.  
XX PD 27-JUN-1991.  
XX PF 07-DEC-1990; 90WO-GB01911.  
XX PR 07-DEC-1990; 90WO-GB01911.  
XX PR 07-DEC-1989; 89GB-0027722.  
XX PA (BRBI-) BRITISH BIO-TECHNOLOGY LTD.  
XX PI Dawson KM, Hunter MG, Czaplewski LG;  
XX PI WPI; 1991-208151/28.  
XX DR N-PSDB; AAQ12160.  
XX PT Fusion protein cleavage by blood clotting enzyme - for prodrn. of  
XX PT fractions having greater antithrombotic activity for therapy and  
XX PT prophylaxis.  
XX PS Disclosure; Page 90; 115pp; English.  
XX CC The streptokinase sequence was obtnd. from PCR amplified chromosomal  
XX CC DNA from S. equisimilis ATCC 10009 or ATCC 9642. The gene was  
XX CC used to construct an expression vector in which two streptokinase

CC genes are linked via a sequence encoding a cleavage site for  
 CC thrombin which, when cleaved, releases the individual proteins  
 CC which have anti-thrombotic activity. The thrombin is present at  
 CC the site of the target thrombus so the active agents are released  
 CC specifically at the place where clot formation is occurring  
 CC See also AAR12887-R12889, AAR12891-R12894, AAR12885 and AAR12522.  
 CC (Updated on 25-MAR-2003 to correct PA field.)  
 CC

SQ Sequence 859 AA;

Query Match 100.0%; Score 30; DB 12; Length 859;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVEY 6  
 |||||  
 DB 178 SVDVEY 183

RESULT 60

AAW21727  
 ID AAW21727 standard; protein; 1181 AA.

XX AC AAW21727;

XX DT 01-OCT-1997 (first entry)

XX DE Streptokinase/maltose binding protein fusion protein, rSKdelta14.  
 XX KW Plasminogen-binding fragment; streptokinase; degradation; MBP;  
 XX KW thrombolytic agent; blood clot; bolus; maltose-binding protein.  
 XX OS Streptococcus equisimilis.

XX FH Key Location/Qualifiers

FT Protein 1..381  
 /label= Maltose binding protein  
 /note= "acts as blocking group"  
 FT Protein 382..1181  
 /label= Modified Streptokinase  
 /note= "Has N-terminal 14 amino acids deleted"

XX PN WO9641883-A1.

XX PD 27-DEC-1996.

XX PF 07-JUN-1996; 96WO-US09640.

XX PR 09-JUN-1995; 95US-0488940.

XX PA (HARD ) HARVARD COLLEGE.

XX PI Reed GL;

XX DR WPI; 1997-065469/06.

XX PT Modified forms of streptokinase resistant to enzymatic cleavage -  
 XX useful as thrombolytic agents in treating thrombosis and in medical  
 XX equipment

XX PS Example 1; Page 12; 65pp; English.

XX CC This sequence represents a fusion protein between maltose-binding  
 CC protein and a mutant form of the the plasminogen-binding fragment  
 CC of streptokinase which has the N-terminal 14 amino acids deleted.  
 CC This fusion protein was used in the design of a modified streptokinase  
 CC has an in vitro degradation rate at least 2 times slower than that of  
 CC native streptokinase. Compounds containing modified streptokinases  
 CC are specifically used as thrombolytic agents for dissolving blood  
 CC clots in vivo in a mammal, preferably at a dose of 20000 U/kg,  
 CC optionally as a bolus rather than by continuous infusion.

XX SQ Sequence 1181 AA;

Query Match 100.0%; Score 30; DB 18; Length 1181;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVEY 6  
 |||||  
 DB 524 SVDVEY 529

RESULT 61

AAW21724  
 ID AAW21724 standard; protein; 1194 AA.

XX AC AAW21724;

XX DT 01-OCT-1997 (first entry)

XX DE Modified streptokinase, rSK5mut.

XX KW plasminogen-binding fragment; streptokinase; degradation; MBP;  
 XX KW thrombolytic agent; blood clot; bolus; maltose-binding protein.

XX OS Streptococcus equisimilis.

XX OS Synthetic.

XX FH Key Location/Qualifiers

FT Protein 1..381  
 /label= Maltose binding protein  
 /note= "acts as blocking group"  
 FT Protein 382..1194  
 /label= Modified streptokinase  
 FT Misc-difference 391  
 /label= R10A  
 FT Misc-difference 417  
 /label= R36A  
 FT Misc-difference 426  
 /label= R45A  
 FT Misc-difference 432  
 /label= R51A  
 FT Misc-difference 440  
 /label= R59A

XX PN WO9641883-A1.

XX PD 27-DEC-1996.

XX PF 07-JUN-1996; 96WO-US09640.

XX PR 09-JUN-1995; 95US-0488940.

XX PA (HARD ) HARVARD COLLEGE.

XX PI Reed GL;

XX DR WPI; 1997-065469/06.

XX PT Modified forms of streptokinase resistant to enzymatic cleavage -  
 XX useful as thrombolytic agents in treating thrombosis and in medical  
 XX equipment

XX PS Claim 15; Page 41-44; 65pp; English.

XX CC This sequence represents a fusion protein between maltose-binding  
 CC protein and a modified form of the plasminogen-binding fragment of  
 CC streptokinase containing 5 point mutations. This modified streptokinase  
 CC has an in vitro degradation rate at least 2 times slower than that of  
 CC native streptokinase. Compounds containing modified streptokinases  
 CC are specifically used as thrombolytic agents for dissolving blood  
 CC clots in vivo in a mammal, preferably at a dose of 20000 U/kg,  
 CC optionally as a bolus rather than by continuous infusion.

XX SQ Sequence 1194 AA;

Query Match 100.0%; Score 30; DB 18; Length 1194;  
Best Local Similarity 100.0%; Pred. No. 2.5e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVEY 6  
|||||

DB 537 SVDVEY 542

RESULT 62  
AAW21726  
ID AAW21726 standard; protein; 1194 AA.  
XX  
XX AC AAW21726;  
XX  
XX DT 01-OCT-1997 (first entry)  
XX  
XX DE Streptokinase/maltose binding protein fusion protein, rSK.  
XX  
XX KW Plasminogen-binding fragment; streptokinase; degradation; MBP;  
XX KW thrombolytic agent; blood clot; bolus; maltose-binding protein.  
XX  
XX OS Streptococcus equisimilis.  
XX  
XX FH Key Location/Qualifiers  
XX FT Protein 1..381  
XX FT /label= Maltose binding protein  
XX FT /note= "acts as blocking group"  
XX FT Protein 382..1194  
XX FT /label= Streptokinase  
XX FT Misc-difference 391  
XX FT /label= R10A  
XX FT Misc-difference 417  
XX FT /label= R36A  
XX FT Misc-difference 426  
XX FT /label= R45A  
XX FT Misc-difference 432  
XX FT /label= R51A  
XX FT Misc-difference 440  
XX FT /label= R59A  
XX FT Misc-difference 766  
XX FT /label= K385A  
XX FT /note= "Given in the specification as K386A"  
XX  
XX PN W09641883-A1.  
XX  
XX PD 27-DEC-1996.  
XX  
XX PF 07-JUN-1996; 96WO-US09640.  
XX  
XX PR 09-JUN-1995; 95US-0488940.  
XX  
XX PA (HARD ) HARVARD COLLEGE.  
XX  
XX PI Reed GL;  
XX  
XX DR WPI; 1997-065469/06.  
XX  
XX PT Modified forms of streptokinase resistant to enzymatic cleavage -  
XX PT useful as thrombolytic agents in treating thrombosis and in medical  
XX PT equipment  
XX  
XX PS Example 1; Page 11-12; 65pp; English.  
XX  
XX CC This sequence represents a fusion protein between maltose-binding  
XX CC protein and the plasminogen-binding fragment of streptokinase.  
XX CC This fusion protein was used in the design of modified streptokinase  
XX CC has an in vitro degradation rate at least 2 times slower than that of  
XX CC native streptokinase. Compounds containing modified streptokinases  
XX CC are specifically used as thrombolytic agents for dissolving blood  
XX CC clots in vivo in a mammal, preferably at a dose of 20000 U/kg,  
XX CC optionally as a bolus rather than by continuous infusion.  
XX  
XX SQ Sequence 1194 AA;

Query Match 100.0%; Score 30; DB 18; Length 1194;  
Best Local Similarity 100.0%; Pred. No. 2.5e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVEY 6  
|||||

DB 537 SVDVEY 542

AAW21725  
ID AAW21725 standard; protein; 1194 AA.  
XX  
XX AC AAW21725;  
XX  
XX DT 01-OCT-1997 (first entry)  
XX  
XX DE Modified streptokinase, rSK6mut.  
XX  
XX KW Plasminogen-binding fragment; streptokinase; degradation; MBP;  
XX KW thrombolytic agent; blood clot; bolus; maltose-binding protein.  
XX  
XX OS Streptococcus equisimilis.  
XX  
XX FH Key Location/Qualifiers  
XX FT Protein 1..381  
XX FT /label= Maltose binding protein  
XX FT /note= "acts as blocking group"  
XX FT Protein 382..1194  
XX FT /label= Modified streptokinase  
XX FT Misc-difference 391  
XX FT /label= R10A  
XX FT Misc-difference 417  
XX FT /label= R36A  
XX FT Misc-difference 426  
XX FT /label= R45A  
XX FT Misc-difference 432  
XX FT /label= R51A  
XX FT Misc-difference 440  
XX FT /label= R59A  
XX FT Misc-difference 766  
XX FT /label= K385A  
XX FT /note= "Given in the specification as K386A"  
XX  
XX PN W09641883-A1.  
XX  
XX PD 27-DEC-1996.  
XX  
XX PF 07-JUN-1996; 96WO-US09640.  
XX  
XX PR 09-JUN-1995; 95US-0488940.  
XX  
XX PA (HARD ) HARVARD COLLEGE.  
XX  
XX PI Reed GL;  
XX  
XX DR WPI; 1997-065469/06.  
XX  
XX PT Modified forms of streptokinase resistant to enzymatic cleavage -  
XX PT useful as thrombolytic agents in treating thrombosis and in medical  
XX PT equipment  
XX  
XX PS Claim 16; Page 44-48; 65pp; English.  
XX  
XX CC This sequence represents a fusion protein between maltose-binding  
XX CC protein and a modified form of the plasminogen-binding fragment of  
XX CC streptokinase containing 6 point mutations. This modified streptokinase  
XX CC has an in vitro degradation rate at least 2 times slower than that of  
XX CC native streptokinase. Compounds containing modified streptokinases  
XX CC are specifically used as thrombolytic agents for dissolving blood  
XX CC clots in vivo in a mammal, preferably at a dose of 20000 U/kg,  
XX CC optionally as a bolus rather than by continuous infusion.  
XX  
XX SQ Sequence 1194 AA;

Query Match 100.0%; Score 30; DB 18; Length 1194;  
Best Local Similarity 100.0%; Pred. No. 2.5e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVEY 6  
|||||

DB 537 SVDVEY 542

Search completed: January 20, 2004, 14:58:47  
Job time : 42 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 20, 2004, 13:54:52 ; Search time 42 Seconds  
(without alignments)  
22.675 Million cell updates/sec

Title: US-09-919-703-1

Perfect score: 30

Sequence: 1 SVDVEY 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 75 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	30	100.0	6	20	AA25009 Streptokinase deri
2	30	100.0	6	23	ABB80001 Streptokinase deri
3	30	100.0	16	23	ABB80005 Streptokinase deri
4	30	100.0	18	20	AA25013 Streptokinase deri
5	30	100.0	20	20	AA25014 Streptokinase deri
6	30	100.0	20	23	ABB80006 Streptokinase deri
7	30	100.0	20	24	ABG76052 Streptokinase frag
8	30	100.0	21	20	AA25015 Streptokinase deri
9	30	100.0	21	23	ABB80007 Streptokinase deri

10	30	100.0	71	20	RAY01550	Antigenic epitope
11	30	100.0	146	20	RAY01558	Peptide correspond
12	30	100.0	150	20	RAY24796	Recombinant strept
13	30	100.0	233	20	RAY01557	Peptide correspond
14	30	100.0	297	16	AA91599	Streptokinase from
15	30	100.0	348	12	AA10196	Streptokinase (1-3
16	30	100.0	356	20	RAY24795	Recombinant strept
17	30	100.0	369	12	AA12892	Truncated Met stre
18	30	100.0	371	12	AA10195	Streptokinase (1-3
19	30	100.0	372	12	AA10197	Streptokinase (1-3
20	30	100.0	372	12	AA10200	Streptokinase (1-3
21	30	100.0	372	21	AA84006	Amino acid sequenc
22	30	100.0	374	12	AA10198	Streptokinase (1-37
23	30	100.0	384	21	AA84007	Amino acid sequenc
24	30	100.0	391	12	AA10199	Streptokinase (1-3
25	30	100.0	401	21	AA84004	Amino acid sequenc
26	30	100.0	413	20	RAY25020	Streptokinase frag
27	30	100.0	413	21	AA84005	Amino acid sequenc
28	30	100.0	413	23	ABB80012	Streptokinase amin
29	30	100.0	413	24	ABG74199	Representative str
30	30	100.0	414	12	AA10194	Streptokinase enco
31	30	100.0	414	13	AA20202	S.equisimilis stre
32	30	100.0	414	15	AA63120	Streptokinase. St
33	30	100.0	414	20	AA24794	Streptococcus equi
34	30	100.0	414	20	RAY01556	Native streptokina
35	30	100.0	414	20	AAW94664	Streptococcus equi
36	30	100.0	414	20	AAW94665	Streptococcus equi
37	30	100.0	414	20	AAW86143	Streptokinase (SK)
38	30	100.0	414	20	AAW86144	De-immunised strep
39	30	100.0	414	21	AA90282	S. equisimilis str
40	30	100.0	414	21	AA801295	Wild type streptok
41	30	100.0	414	21	AA801296	Altered streptokina
42	30	100.0	414	22	AA874940	Mutant streptokina
43	30	100.0	415	21	AA99593	Streptococcus plas
44	30	100.0	415	21	AA950870	Streptococcus sp.
45	30	100.0	440	6	AA50620	Sequence encoded b
46	30	100.0	440	11	AA806378	Streptokinase A fr
47	30	100.0	440	11	AA806377	Streptokinase G pr
48	30	100.0	440	12	AA12889	Streptokinase. St
49	30	100.0	440	23	ABP29561	Streptococcus poly
50	30	100.0	483	12	AA12885	Factor Xa-cleavabl
51	30	100.0	483	12	AA12522	Factor Xa-cleavabl
52	30	100.0	499	12	AA12891	Streptokinase fuse
53	30	100.0	531	12	AA11829	FB-FB-SK fusion co
54	30	100.0	736	20	AA24798	Recombinant strept
55	30	100.0	747	12	AA12894	Met-core streptoki
56	30	100.0	795	20	AA24797	Streptokinase and
57	30	100.0	800	18	AAW21723	Plasminogen-bindin
58	30	100.0	813	18	AAW21728	Wild type plasmino
59	30	100.0	859	12	AA12893	OmpAL streptokinas
60	30	100.0	1181	18	AAW21727	Streptokinase/malt
61	30	100.0	1194	18	AAW21724	Modified streptoki
62	30	100.0	1194	18	AAW21726	Streptokinase/malt
63	30	100.0	1194	18	AAW21725	Modified streptoki
64	29	96.7	520	22	ABB66301	Drosophila melanog
65	29	96.7	1190	22	ABB58817	Drosophila melanog
66	27	90.0	6	20	AA25011	Streptokinase deri
67	27	90.0	6	23	ABB80003	Streptokinase deri
68	27	90.0	6	24	ABG74195	Streptokinase frag
69	27	90.0	17	21	AA51961	P. pastoris lysyl
70	27	90.0	17	21	AA51973	P. pastoris lysyl
71	27	90.0	17	24	ABP60417	Pichia pastoris ly
72	27	90.0	223	22	AAU64792	Protonibacterium
73	27	90.0	313	22	ABG16037	Novel human diagn
74	27	90.0	355	18	AAW06741	Leptospira membran
75	27	90.0	391	24	ABR39091	Calid herpesvirus

ALIGNMENTS

RESULT 1  
AA25009

ID AAY25009 standard; peptide; 6 AA.  
 XX AAY25009;  
 AC  
 XX  
 DT 23-AUG-1999 (first entry)  
 XX  
 DE Streptokinase derived peptide 1 for amelioration of cell death.  
 KW Streptokinase; cell death; amelioration; treatment; disease; aging; AIDS;  
 KW cellular differentiation; physical insult; trauma; anoxia; hyperthermia;  
 KW hypothermia; brain; spinal cord; kidney; heart; lung; liver; skin; HIV;  
 KW viral disorder; hepatitis; retroviral; infection; encephalitis; FALS;  
 KW neurodegenerative disorder; Parkinson's disease; Alzheimer's disease;  
 KW Huntington's disease; cerebellar degeneration; cardiovascular disease;  
 KW familial amyotrophic lateral sclerosis; atherosclerosis; heart failure;  
 KW infarction; heart disease; cardiomyopathy; hypertensive; myocardial;  
 KW reperfusion injury; immune disease; rheumatoid arthritis; renal; retinal;  
 KW systemic lupus erythematosus; insulin-dependent; diabetes mellitus;  
 KW pernicious anaemia; dermatomyositis; erythema nodosum; myasthenia gravis;  
 KW Sjogren's syndrome; temporal arthritis; autoimmune polyarthritides;  
 KW Wegener's granulomatosis; glomerulonephritis; anti-phospholipid syndrome;  
 KW neoplastic disorder; leukemia; sarcoma; myeloma; carcinoma; neuroma;  
 KW melanoma; cancer; breast; colon; cervix; prostate; Hodgkin's disease;  
 KW non-Hodgkin's lymphoma; inflammatory disorder; stroke; ischemia;  
 KW spinal cord; toxic insult; pulmonary; macular degeneration; cataract;  
 KW pancreatitis; Crohn's disease; ulcerative colitis; motor neuron disease;  
 KW Guillan Bare Syndrome; demyelinating disease; bypass surgery;  
 KW chemotherapy; Clozapine; AZT; anthracycline.  
 XX  
 OS Synthetic.  
 XX  
 FN US5917013-A.  
 XX  
 PD 29-JUN-1999.  
 XX  
 PF 05-DEC-1996; 96US-07595599.  
 XX  
 PR 06-DEC-1995; 95US-0008233.  
 XX  
 PR 05-DEC-1996; 96US-07595599.  
 XX  
 PA (RABK/) RABKIN S W.  
 XX  
 PI Krystal G, Rabkin SW;  
 XX  
 DR WPI; 1999-394231/33.  
 XX  
 PT Peptides that ameliorate cell death useful for treating conditions  
 XX associated with cellular differentiation  
 PS Claim 2; Column 12; 15pp; English.  
 XX  
 CC AAY25009-Y25019 are novel peptides derived from streptokinase that  
 CC ameliorate cell death. The products of the invention and their encoding  
 CC nucleic acids may be useful for treating diseases and conditions related  
 CC to aging, cellular differentiation, physical insult (e.g. physical  
 CC trauma, anoxia, hyperthermia, hypothermia, chemically induced damage,  
 CC and trauma to the brain, spinal cord, kidney, heart, lungs, liver, skin  
 CC and any other organ), viral disorders (e.g. hepatitis, retroviral  
 CC infections, viral encephalitis, and AIDS/HIV), neurodegenerative  
 CC disorders (e.g. Parkinson's disease, Alzheimer's disease, Huntington's  
 CC disease, cerebellar degenerations, and familial amyotrophic lateral  
 CC sclerosis (FALS)), cardiovascular disease (e.g. atherosclerosis,  
 CC myocardial infarction, heart failure, cardiomyopathy, myocardial  
 CC reperfusion injury, and hypertensive heart disease), immune disease (e.g.  
 CC rheumatoid arthritis, systemic lupus erythematosus, insulin-dependent,  
 CC diabetes mellitus, lupus, pernicious anaemia, dermatomyositis, erythema  
 CC nodosum, Sjogren's syndrome, temporal arthritis, myasthenia gravis,  
 CC Wegener's granulomatosis, glomerulonephritis, anti-phospholipid syndrome,  
 CC sarcomas, myelomas, carcinomas, neuromas, melanoma, cancers of the  
 CC breast, brain, colon, cervix, and prostate, Hodgkin's disease and  
 CC non-Hodgkin's lymphoma), inflammatory disorders (e.g. inflammatory joint  
 CC disorders and inflammatory induced cell damage to the eye, brain and

CC other organs), ischemia or reperfusion injury (e.g. myocardial ischemia  
 CC and reperfusion injury, renal ischemia, spinal cord ischemia and/or  
 CC reperfusion injury, retinal ischemia or infarction, and stroke), toxic  
 CC insult (e.g. liver toxicity, pulmonary toxicity, toxic damage to other  
 CC organs from chemicals, radiation, and other noxious substances), macular  
 CC degeneration, cataract formation, pancreatitis, Crohn's disease,  
 CC ulcerative colitis, accelerated aging, spinal cord disease (e.g. motor  
 CC neuron diseases, degeneration of the spinal cord, Guillan Bare Syndrome  
 CC and demyelinating disease), bypass surgery, chemotherapy,  
 CC chemically-induced reperfusion, and therapeutics such as clozapine, AZT,  
 CC and anthracyclines.  
 XX  
 SQ Sequence 6 AA;  
 Query Match 100.0%; Score 30; DB 20; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SVDVEY 6  
 Db 1 SVDVEY 6  
 RESULT 2  
 ID ABB80001 standard; peptide; 6 AA.  
 XX ABB80001;  
 AC ABB80001;  
 XX  
 DT 26-JUL-2002 (first entry)  
 XX  
 DE Streptokinase derived peptide#1.  
 XX  
 KW Streptokinase; cell death; apoptosis; necrosis; neurotropic;  
 KW neuroprotective; antiparkinsonian; anticonvulsant; cytostatic;  
 KW antiinflammatory; antiarthritic; antirheumatic; cardiant;  
 KW antiatherosclerotic; vasotropic; immunosuppressive; anti-HIV;  
 KW dermatological; antidiabetic; antianemic; virucide; ophthalmological;  
 KW Parkinson's disease; Alzheimer's disease; Huntington's disease;  
 KW anticancer; antibacterial; antiparasitic; neurodegenerative disease;  
 KW cerebellar degeneration; neoplastic disorder; cancer;  
 KW inflammatory disorder; arthritis; inflammatory joint disorders;  
 KW cardiovascular disease; heart failure; atherosclerosis;  
 KW myocardial reperfusion injury; immune disease; autoimmune disease;  
 KW acquired immunodeficiency syndrome; AIDS; rheumatoid arthritis;  
 KW systemic lupus erythematosus; diabetes mellitus; pernicious anaemia;  
 KW myelodegenerative diseases; viral diseases; macular degeneration;  
 KW cataract; Crohn's disease; ulcerative colitis; pancreatitis;  
 KW prion disease; aging.  
 XX  
 OS Synthetic.  
 XX  
 PN US6348567-B1.  
 XX  
 PD 19-FEB-2002.  
 XX  
 PF 19-APR-1999; 99US-0294457.  
 XX  
 PR 06-DEC-1995; 95US-008233P.  
 XX  
 PR 05-DEC-1996; 96US-0759599.  
 XX  
 PA (MOLE-) MOLECULAR THERAPEUTICS INC.  
 XX  
 PI Krystal G, Rabkin SW;  
 XX  
 DR WPI; 2002-266542/31.  
 XX  
 PT New peptides obtained from streptokinase, useful in ameliorating cell  
 XX death due to apoptosis and/or necrosis and treating neurodegenerative,  
 XX neoplastic, immune, cardiovascular and inflammatory disorders  
 PS Claim 3; Column 5; 18pp; English.  
 XX

CC The invention relates to an isolated peptide obtained from streptokinase,  
CC or its derivative or analog, which ameliorate cell death. The activity of  
CC peptides of the invention may be described as, neurotropic,  
CC neuroprotective, antiparkinsonian, anticonvulsant, cytostatic,  
CC antiinflammatory, antiarthritic, antirheumatic, cardiac,  
CC antiatherosclerotic, vasotropic, immunosuppressive, anti-HIV,  
CC dermatological, antidiabetic, antianaemic, virucide, ophthalmological,  
CC antiulcer, antibacterial and antiparasitic. Peptides of the invention  
CC ameliorates apoptosis and necrosis in a warm-blooded animal. Compositions  
CC comprising peptides of the invention are useful for treating  
CC neurodegenerative diseases (e.g. Parkinson's, Alzheimer's, Huntington's  
CC disease and cerebellar degeneration) neoplastic disorders including  
CC cancer, inflammatory disorders (e.g. arthritis, inflammatory joint  
CC disorders), cardiovascular diseases (e.g. heart failure, atherosclerosis  
CC and myocardial reperfusion injury), immune diseases (e.g. autoimmune  
CC disease, acquired immunodeficiency syndrome (AIDS), rheumatoid arthritis,  
CC systemic lupus erythematosus, diabetes mellitus, pernicious anaemia),  
CC myelodegenerative diseases, viral diseases, and degenerative diseases of  
CC any organ. Other disorders include macular degeneration, cataracts,  
CC Crohn's disease, ulcerative colitis, cataracts, pancreatitis, infectious  
CC diseases including bacterial, parasite, prion-based diseases, and  
CC accelerated aging. The current sequence represents a streptokinase  
CC derived peptide of the invention with an ability to ameliorate cell  
CC death in cardiac myocytes.  
XX Sequence 6 AA;

Query Match 100.0%; Score 30; DB 23; Length 6;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVDVEY 6  
| | | | |  
Db 1 SVDVEY 6

RESULT 3  
ABB90005  
ID ABB80005 standard; peptide; 16 AA.  
XX  
AC ABB80005;  
XX  
DT 26-JUL-2002 (first entry)  
XX  
DE Streptokinase derived peptide#5.

XX Streptokinase; cell death; apoptosis; necrosis; neurotropic;  
KW neuroprotective; antiparkinsonian; anticonvulsant; cytostatic;  
KW antiinflammatory; antiarthritic; antirheumatic; cardiac;  
KW antiatherosclerotic; vasotropic; immunosuppressive; anti-HIV;  
KW dermatological; antidiabetic; antianaemic; virucide; ophthalmological;  
KW antiulcer; antibacterial; antiparasitic; neurodegenerative disease;  
KW Parkinson's disease; Alzheimer's disease; Huntington's disease;  
KW cerebellar degeneration; neoplastic disorder; cancer;  
KW inflammatory disorder; arthritis; inflammatory joint disorders;  
KW cardiovascular disease; heart failure; atherosclerosis;  
KW myocardial reperfusion injury; immune disease; autoimmune disease;  
KW acquired immunodeficiency syndrome; AIDS; rheumatoid arthritis;  
KW systemic lupus erythematosus; diabetes mellitus; pernicious anaemia;  
KW myelodegenerative diseases; viral diseases; macular degeneration;  
KW cataract; Crohn's disease; ulcerative colitis; pancreatitis;  
KW prion disease; aging.

OS Synthetic.  
XX  
XX US6348567-B1.  
PN  
XX  
PD 19-FEB-2002.  
XX  
XX 19-APR-1999; 99US-0294457.  
PF  
XX 06-DEC-1995; 95US-008233P.  
PR  
XX 05-DEC-1996; 96US-0759599.

XX (MOLE-) MOLECULAR THERAPEUTICS INC.  
PA Krystal G, Rabkin SW;  
XX WPI; 2002-266542/31.  
DR  
XX New peptides obtained from streptokinase, useful in ameliorating cell  
PT death due to apoptosis and/or necrosis and treating neurodegenerative,  
PT neoplastic, immune, cardiovascular and inflammatory disorders -  
XX Claim 7; Column 5; 18pp; English.  
PS  
XX The invention relates to an isolated peptide obtained from streptokinase,  
CC or its derivative or analog, which ameliorate cell death. The activity of  
CC peptides of the invention may be described as, neurotropic,  
CC neuroprotective, antiparkinsonian, anticonvulsant, cytostatic,  
CC antiinflammatory, antiarthritic, antirheumatic, cardiac,  
CC antiatherosclerotic, vasotropic, immunosuppressive, anti-HIV,  
CC dermatological, antidiabetic, antianaemic, virucide, ophthalmological,  
CC antiulcer, antibacterial and antiparasitic. Peptides of the invention  
CC ameliorates apoptosis and necrosis in a warm-blooded animal. Compositions  
CC comprising peptides of the invention are useful for treating  
CC neurodegenerative diseases (e.g. Parkinson's, Alzheimer's, Huntington's  
CC disease and cerebellar degeneration) neoplastic disorders including  
CC cancer, inflammatory disorders (e.g. arthritis, inflammatory joint  
CC disorders), cardiovascular diseases (e.g. heart failure, atherosclerosis  
CC and myocardial reperfusion injury), immune diseases (e.g. autoimmune  
CC disease, acquired immunodeficiency syndrome (AIDS), rheumatoid arthritis,  
CC systemic lupus erythematosus, diabetes mellitus, pernicious anaemia),  
CC myelodegenerative diseases, viral diseases, and degenerative diseases of  
CC any organ. Other disorders include macular degeneration, cataracts,  
CC Crohn's disease, ulcerative colitis, cataracts, pancreatitis, infectious  
CC diseases including bacterial, parasite, prion-based diseases, and  
CC accelerated aging. The current sequence represents a streptokinase  
CC derived peptide of the invention with an ability to ameliorate cell  
CC death in cardiac myocytes.  
XX Sequence 16 AA;

Query Match 100.0%; Score 30; DB 23; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.9;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVDVEY 6  
| | | | |  
Db 1 SVDVEY 6

RESULT 4  
AAV25013  
ID AAV25013 standard; peptide; 18 AA.  
XX  
AC AAV25013;  
XX  
DT 23-AUG-1999 (first entry)  
XX  
DE Streptokinase derived peptide 5 for amelioration of cell death.

XX Streptokinase; cell death; amelioration; treatment; disease; aging; AIDS;  
KW cellular differentiation; physical insult; trauma; anoxia; hyperthermia;  
KW hypothermia; brain; spinal cord; kidney; heart; lung; liver; skin; HIV;  
KW viral disorder; hepatitis; retroviral; infection; encephalitis; FALS;  
KW neurodegenerative disorder; Parkinson's disease; Alzheimer's disease;  
KW Huntington's disease; cerebellar degeneration; cardiovascular disease;  
KW familial amyotrophic lateral sclerosis; atherosclerosis; heart failure;  
KW infarction; heart disease; cardiomyopathy; hypertensive; myocardial;  
KW reperfusion injury; immune disease; rheumatoid arthritis; renal; retinal;  
KW systemic lupus erythematosus; insulin-dependent; diabetes mellitus;  
KW pernicious anaemia; dermatomyositis; myethema nodosum; myasthenia gravis;  
KW Sjogren's syndrome; temporal arthritis; autoimmune polyarthritides;  
KW Wegener's granulomatosis; glomerulonephritis; anti-phospholipid syndrome;  
KW neoplastic disorder; leukemia; sarcoma; myeloma; carcinoma; neuroma;

KW melanoma; cancer; breast; colon; cervix; prostate; Hodgkin's disease;  
 KW non-Hodgkin's lymphoma; inflammatory disorder; stroke; ischemia;  
 KW spinal cord; toxic insult; pulmonary; macular degeneration; cataract;  
 KW pancreatitis; Crohn's disease; ulcerative colitis; motor neuron disease;  
 KW Guillan Bare Syndrome; demyelinating disease; bypass surgery;  
 KW chemotherapy; clozapine; AZT; anthracycline.

XX Synthetic.

OS US5917013-A.

PN 29-JUN-1999.

PD 05-DEC-1996; 96US-0759599.

PF 06-DEC-1995; 95US-0008233.

PR 05-DEC-1996; 96US-0759599.

XX (RABK/) RABKIN S W.

PI Krystal G, Rabkin SW;

XX WPI; 1999-394231/33.

DR Peptides that ameliorate cell death useful for treating conditions  
 associated with cellular differentiation

XX Claim 6; Column 12; 15pp; English.

XX AA25009-Y25019 are novel peptides derived from streptokinase that  
 CC ameliorate cell death. The products of the invention and their encoding  
 CC nucleic acids may be useful for treating diseases and conditions related  
 CC to aging, cellular differentiation, physical insult (e.g. physical  
 CC trauma, anoxia, hyperthermia, hypothermia, chemically induced damage,  
 CC and trauma to the brain, spinal cord, kidney, heart, lungs, liver, skin  
 CC and any other organ), viral disorders (e.g. hepatitis, retroviral  
 CC infections, viral encephalitis, and AIDS/HIV), neurodegenerative  
 CC disorders (e.g. Parkinson's disease, Alzheimer's disease, Huntington's  
 CC disease, cerebellar degenerations, and familial amyotrophic lateral  
 CC sclerosis (FALS)), cardiovascular disease (e.g. atherosclerosis,  
 CC myocardial infarction, heart failure, cardiomyopathy, myocardial  
 CC reperfusion injury, and hypertensive heart disease), immune disease (e.g.  
 CC rheumatoid arthritis, systemic lupus erythematosus, insulin-dependent,  
 CC diabetes mellitus, lupus, pernicious anaemia, dermatomyositis, erythema  
 CC nodosum, Sjogren's syndrome, temporal arthritis, myasthenia gravis,  
 CC Wegener's granulomatosis, glomerulonephritis, anti-phospholipid syndrome,  
 CC sarcomas, myelomas, carcinomas, neuromas, melanoma, cancers of the  
 CC breast, brain, colon, cervix, and prostate, Hodgkin's disease and  
 CC non-Hodgkin's lymphoma), inflammatory disorders (e.g. inflammatory joint  
 CC disorders and inflammatory induced cell damage to the eye, brain and  
 CC other organs), ischemia or reperfusion injury (e.g. myocardial ischemia  
 CC and reperfusion injury, renal ischemia, spinal cord ischemia and/or  
 CC reperfusion injury, retinal ischemia or infarction, and stroke), toxic  
 CC insult (e.g. liver toxicity, pulmonary toxicity, toxic damage to other  
 CC organs from chemicals, radiation, and other noxious substances), macular  
 CC degeneration, cataract formation, pancreatitis, Crohn's disease,  
 CC ulcerative colitis, accelerated aging, spinal cord disease (e.g. motor  
 CC neuron diseases, degeneration of the spinal cord, Guillan Bare Syndrome  
 CC and demyelinating disease), bypass surgery, chemotherapy,  
 CC chemically-induced reperfusion, and therapeutics such as clozapine, AZT,  
 CC and anthracyclines.

XX Sequence 18 AA;

Query Match 100.0%; Score 30; DB 20; Length 18;

Best Local Similarity 100.0%; Pred. No. 2,2;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVDVEY 6

Db 1 SVDVEY 6

RESULT 5

AA25014

ID AA25014 standard; peptide; 20 AA.

XX AA25014;

AC AA25014;

XX 23-AUG-1999 (first entry)

XX Streptokinase derived peptide 6 for amelioration of cell death.

XX Streptokinase; cell death; amelioration; treatment; disease; aging; AIDS;  
 KW cellular differentiation; physical insult; trauma; anoxia; hyperthermia;  
 KW hypothermia; brain; spinal cord; kidney; heart; lung; liver; skin; HIV;  
 KW viral disorder; hepatitis; retroviral; infection; encephalitis; FALS;  
 KW neurodegenerative disorder; Parkinson's disease; Alzheimer's disease;  
 KW Huntington's disease; cerebellar degeneration; cardiovascular disease;  
 KW familial amyotrophic lateral sclerosis; atherosclerosis; heart failure;  
 KW infarction; heart disease; cardiomyopathy; hypertensive; myocardial;  
 KW reperfusion injury; immune disease; rheumatoid arthritis; renal; retinal;  
 KW systemic lupus erythematosus; insulin-dependent; diabetes mellitus;  
 KW pernicious anaemia; dermatomyositis; myasthenia gravis;  
 KW Sjogren's syndrome; temporal arthritis; autoimmune polyarthritides;  
 KW Wegener's granulomatosis; glomerulonephritis; anti-phospholipid syndrome;  
 KW neoplastic disorder; leukemia; sarcoma; myeloma; carcinoma; neuroma;  
 KW melanoma; cancer; breast; colon; cervix; prostate; Hodgkin's disease;  
 KW non-Hodgkin's lymphoma; inflammatory disorder; stroke; ischemia;  
 KW spinal cord; toxic insult; pulmonary; macular degeneration; cataract;  
 KW pancreatitis; Crohn's disease; ulcerative colitis; motor neuron disease;  
 KW Guillan Bare Syndrome; demyelinating disease; bypass surgery;  
 KW chemotherapy; clozapine; AZT; anthracycline.

XX Synthetic.

XX US5917013-A.

XX 29-JUN-1999.

PD 05-DEC-1996; 96US-0759599.

PR 06-DEC-1995; 95US-0008233.

PR 05-DEC-1996; 96US-0759599.

XX (RABK/) RABKIN S W.

PI Krystal G, Rabkin SW;

XX WPI; 1999-394231/33.

XX Peptides that ameliorate cell death useful for treating conditions  
 associated with cellular differentiation

XX Claim 7; Column 12; 15pp; English.

XX AA25009-Y25019 are novel peptides derived from streptokinase that  
 CC ameliorate cell death. The products of the invention and their encoding  
 CC nucleic acids may be useful for treating diseases and conditions related  
 CC to aging, cellular differentiation, physical insult (e.g. physical  
 CC trauma, anoxia, hyperthermia, hypothermia, chemically induced damage,  
 CC and trauma to the brain, spinal cord, kidney, heart, lungs, liver, skin  
 CC and any other organ), viral disorders (e.g. hepatitis, retroviral  
 CC infections, viral encephalitis, and AIDS/HIV), neurodegenerative  
 CC disorders (e.g. Parkinson's disease, Alzheimer's disease, Huntington's  
 CC disease, cerebellar degenerations, and familial amyotrophic lateral  
 CC sclerosis (FALS)), cardiovascular disease (e.g. atherosclerosis,  
 CC myocardial infarction, heart failure, cardiomyopathy, myocardial  
 CC reperfusion injury, and hypertensive heart disease), immune disease (e.g.  
 CC rheumatoid arthritis, systemic lupus erythematosus, insulin-dependent,  
 CC diabetes mellitus, lupus, pernicious anaemia, dermatomyositis, erythema  
 CC nodosum, Sjogren's syndrome, temporal arthritis, myasthenia gravis,  
 CC Wegener's granulomatosis, glomerulonephritis, anti-phospholipid syndrome,  
 CC sarcomas, myelomas, carcinomas, neuromas, melanoma, cancers of the

CC breast, brain, colon, cervix, and prostate, Hodgkin's disease and  
 CC non-Hodgkin's lymphoma), inflammatory disorders (e.g. inflammatory joint  
 CC disorders and inflammation induced cell damage to the eye, brain and  
 CC other organs), ischemia or reperfusion injury (e.g. myocardial ischemia  
 CC and reperfusion injury, renal ischemia, spinal cord ischemia and/or  
 CC reperfusion injury, retinal ischemia or infarction, and stroke), toxic  
 CC insult (e.g. liver toxicity, pulmonary toxicity, toxic damage to other  
 CC organs from chemicals, radiation, and other noxious substances), macular  
 CC degeneration, cataract formation, pancreatitis, Crohn's disease,  
 CC ulcerative colitis, accelerated aging, spinal cord disease (e.g. motor  
 CC neuron diseases, degeneration of the spinal cord, Guillain Barre Syndrome  
 CC and demyelinating disease), bypass surgery, chemotherapy,  
 CC chemically-induced reperfusion, and therapeutics such as clozapine, AZT,  
 CC and antithyroidal drugs.  
 XX  
 SQ Sequence 20 AA;  
 Query Match 100.0%; Score 30; DB 20; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 2.4;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SVDVEY 6  
 Db |||||  
 1 SVDVEY 6  
 RESULT 6  
 ABB80006  
 ID ABB80006 standard; peptide; 20 AA.  
 XX  
 AC ABB80006;  
 XX  
 DT 26-JUL-2002 (first entry)  
 XX  
 DE Streptokinase derived peptide#6.  
 XX  
 KW Streptokinase; cell death; apoptosis; necrosis; neurotropic;  
 KW neuroprotective; antiparkinsonian; anticonvulsant; cytostatic;  
 KW antiinflammatory; antiarthritic; antirheumatic; cardiant;  
 KW antiatherosclerotic; vasotropic; immunosuppressive; anti-HIV;  
 KW dermatological; antidiabetic; antianaemic; virucide; ophthalmological;  
 KW antitumor; antibacterial; antiparasitic; neurodegenerative disease;  
 KW Parkinson's disease; Alzheimer's disease; Huntington's disease;  
 KW cerebellar degeneration; neoplastic disorder; cancer;  
 KW inflammatory disorder; arthritis; inflammatory joint disorders;  
 KW cardiovascular disease; heart failure; atherosclerosis;  
 KW myocardial reperfusion injury; immune disease; autoimmune disease;  
 KW acquired immunodeficiency syndrome; AIDS; rheumatoid arthritis;  
 KW systemic lupus erythematosus; diabetes mellitus; pernicious anaemia;  
 KW myelodegenerative diseases; viral diseases; macular degeneration;  
 KW cataract; Crohn's disease; ulcerative colitis; pancreatitis;  
 KW prion disease; aging.  
 XX  
 OS Synthetic.  
 XX  
 XX US6348567-B1.  
 XX  
 XX 19-FEB-2002.  
 XX  
 XX 19-APR-1999; 99US-0294457.  
 XX  
 XX 06-DEC-1995; 95US-008233P.  
 XX  
 XX 03-DEC-1996; 96US-0759599.  
 XX  
 XX (MOLE-) MOLECULAR THERAPEUTICS INC.  
 XX  
 XX Krystal G, Rabkin SW;  
 XX  
 XX WPI; 2002-266542/31.  
 XX  
 XX New peptides obtained from streptokinase, useful in ameliorating cell  
 XX death due to apoptosis and/or necrosis and treating neurodegenerative,  
 XX neoplastic, immune, cardiovascular and inflammatory disorders -

XX Claim 8; Column 5; 18pp; English.  
 PS The invention relates to an isolated peptide obtained from streptokinase,  
 CC or its derivative or analog, which ameliorate cell death. The activity of  
 CC peptides of the invention may be described as, neurotropic,  
 CC neuroprotective, antiparkinsonian, anticonvulsant, cytostatic,  
 CC antiinflammatory, antiarthritic, antirheumatic, cardiant,  
 CC antiatherosclerotic, vasotropic, immunosuppressive, anti-HIV,  
 CC dermatological, antidiabetic, antianaemic, virucide, ophthalmological,  
 CC antitumor, antibacterial and antiparasitic. Peptides of the invention  
 CC ameliorates apoptosis and necrosis in a warm-blooded animal. Compositions  
 CC comprising peptides of the invention are useful for treating  
 CC neurodegenerative diseases (e.g. Parkinson's, Alzheimer's, Huntington's  
 CC disease and cerebellar degeneration) neoplastic disorders including  
 CC cancer, inflammatory disorders (e.g. arthritis, inflammatory joint  
 CC disorders), cardiovascular diseases (e.g. heart failure, atherosclerosis  
 CC and myocardial reperfusion injury), immune diseases (e.g. autoimmune  
 CC disease, acquired immunodeficiency syndrome (AIDS), rheumatoid arthritis,  
 CC systemic lupus erythematosus, diabetes mellitus, pernicious anaemia),  
 CC myelodegenerative diseases, viral diseases, and degenerative diseases of  
 CC any organ. Other disorders include macular degeneration, cataracts,  
 CC Crohn's disease, ulcerative colitis, cataracts, pancreatitis, infectious  
 CC diseases including bacteria, parasite, prion-based diseases, and  
 CC accelerated aging. The current sequence represents a streptokinase  
 CC derived peptide of the invention with an ability to ameliorate cell  
 CC death in cardiac myocytes.  
 XX  
 SQ Sequence 20 AA;  
 Query Match 100.0%; Score 30; DB 23; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 2.4;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SVDVEY 6  
 Db |||||  
 1 SVDVEY 6  
 RESULT 7  
 ABB76052  
 ID ABB76052 standard; peptide; 20 AA.  
 XX  
 AC ABB76052;  
 XX  
 DT 20-MAY-2003 (first entry)  
 XX  
 DE Streptokinase fragment based, cell death ameliorating, 20mer peptide.  
 XX  
 KW Cell death; streptokinase; neurodegenerative disorder; leukaemia; AIDS;  
 KW Parkinson's disease; Alzheimer's disease; cardiovascular disease; trauma;  
 KW atherosclerosis; myocardial infarction; immune disease; carcinoma;  
 KW rheumatoid arthritis; neoplastic disorder; inflammatory disorder;  
 KW arthritis; inflammatory induced cell damage; motor neuron disease;  
 KW physical insult; severe shock; ischaemia; reperfusion injury; hepatitis;  
 KW cell death associated procedure; spinal cord reperfusion injury;  
 KW toxic insult; liver toxicity; pulmonary toxicity; spinal cord disease;  
 KW Guillain-Barre syndrome; bypass surgery; myocardial ischaemia;  
 KW chemotherapy; viral disease; viral encephalitis; infectious disease;  
 KW bacterial disease; prion-based disease; macular degeneration;  
 KW cataract formation; pancreatitis; Crohn's disease; ulcerative colitis;  
 KW accelerated aging; oxidative stress.  
 XX  
 OS Synthetic.  
 XX  
 XX US2002165129-A1.  
 XX  
 XX 07-NOV-2002.  
 XX  
 XX 31-JUL-2001; 2001US-0919703.  
 XX  
 XX 06-DEC-1995; 95US-008233P.  
 XX  
 XX 19-APR-1999; 99US-0294457.

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PR 05-DEC-1996; 96US-0759599.
XX (KRYSTAL) KRYSTAL G.
PA (RABKIN) RABKIN S W.
XX
XX Krystal G, Rabkin SW;
XX WPI; 2003-246673/25.
DR
XX
XX Pharmaceutical composition for treating e.g. neurodegenerative
PT disorder, cardiovascular disease, neoplastic disease, viral disease
PT and immune diseases, comprises a peptide capable of ameliorating cell
PT death
XX
XX Claim 2; Page 3; 19pp; English.
PS
XX
XX The invention relates to a pharmaceutical composition, which comprises a
CC peptide capable of ameliorating cell death, its derivative or analogue,
CC comprising a sequence Val-Asp-Val, where the peptide is in a suitable
CC pharmaceutical carrier or diluent. The pharmaceutical composition
CC (comprising the peptide) is useful for treating or preventing cell
CC death associated with a neurodegenerative disorder e.g. Parkinson's
CC disease and Alzheimer's disease; cardiovascular disease e.g.
CC atherosclerosis and myocardial infarction; immune disease e.g. AIDS and
CC rheumatoid arthritis; neoplastic disorders e.g. leukaemia and carcinoma;
CC inflammatory disorder e.g. arthritis and inflammatory induced cell
CC damage; disease caused by physical insult e.g. trauma and severe shock;
CC ischaemia or reperfusion injury e.g. myocardial ischaemia and spinal cord
CC reperfusion injury; toxic insult e.g. liver toxicity and pulmonary
CC toxicity; spinal cord disease e.g. motor neuron disease and Guillain-Barre
CC syndrome; procedures associated with cell death e.g. bypass surgery and
CC chemotherapy; viral disease e.g. hepatitis and viral encephalitis;
CC infectious diseases e.g. bacterial disease and prion-based disease;
CC macular degeneration; cataract formation; pancreatitis; Crohn's disease;
CC ulcerative colitis; accelerated aging and oxidative stress in a warm-
CC blooded animal. The present sequence represents the amino acid sequence
CC of a 20mer peptide capable of ameliorating cell death which is based on a
XX streptokinase fragment.
XX
XX Sequence 20 AA;
XX
XX Query Match 100.0%; Score 30; DB 24; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 2.4;
XX Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 SVDVEY 6
XX DB 1 SVDVEY 6
XX
XX RESULT 8
XX AAY25015
XX ID AAY25015 standard; peptide; 21 AA.
XX AC AAY25015;
XX
XX DT 23-AUG-1999 (first entry)
XX
XX Streptokinase derived peptide 7 for amelioration of cell death.
XX
XX Streptokinase; cell death; amelioration; treatment; disease; aging; AIDS;
XX cellular differentiation; physical insult; trauma; anoxia; hyperthermia;
XX hypothermia; brain; spinal cord; kidney; heart; lung; liver; skin; HIV;
XX viral disorder; hepatitis; retroviral; infection; encephalitis; FALS;
XX neurodegenerative disorder; Parkinson's disease; Alzheimer's disease;
XX Huntington's disease; cerebellar degeneration; cardiovascular disease;
XX familial amyotrophic lateral sclerosis; atherosclerosis; heart failure;
XX infarction; heart disease; cardiomyopathy; hypertensive; myocardial;
XX reperfusion injury; immune disease; rheumatoid arthritis; renal; retinal;
XX systemic lupus erythematosus; insulin-dependent diabetes mellitus;
XX Sjogren's syndrome; dermatomyositis; enythema nodosum; myasthenia gravis;
XX Wegener's granulomatosis; glomerulonephritis; anti-phospholipid syndrome;

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KW neoplastic disorder; leukemia; sarcoma; myeloma; carcinoma; neuroma;
KW melanoma; cancer; breast; colon; cervix; prostate; stroke; ischemia;
KW non-Hodgkin's lymphoma; inflammatory disorder; stroke; ischemia;
KW spinal cord; toxic insult; pulmonary disorder; macular degeneration; cataract;
KW pancreatitis, Crohn's disease; ulcerative colitis; motor neuron disease;
KW Guillan Bare Syndrome; demyelinating disease; bypass surgery;
KW chemotherapy; clozapine; AZT; anthracycline.
XX
XX Synthetic.
XX
XX US5917013-A.
XX
XX 29-JUN-1999.
XX
XX 05-DEC-1996; 96US-0759599.
XX
XX 06-DEC-1995; 95US-0008233.
XX 03-DEC-1996; 96US-0759599.
XX (RABKIN) RABKIN S W.
XX
XX Krystal G, Rabkin SW;
XX WPI; 1999-394231/33.
XX
XX Peptides that ameliorate cell death useful for treating conditions
XX associated with cellular differentiation
XX
XX Claim 8; Column 12; 15pp; English.
XX
XX AAY25009-Y25019 are novel peptides derived from streptokinase that
XX ameliorate cell death. The products of the invention and their encoding
XX nucleic acids may be useful for treating diseases and conditions related
XX to aging, cellular differentiation, physical insult (e.g. physical
XX trauma, anoxia, hyperthermia, hypothermia, chemically induced damage,
XX and trauma to the brain, spinal cord, kidney, heart, lungs, liver, skin
XX and any other organ), viral disorders (e.g. hepatitis, retroviral
XX infections, viral encephalitis, and AIDS/HIV), neurodegenerative
XX disorders (e.g. Parkinson's disease, Alzheimer's disease, Huntington's
XX disease, cerebellar degenerations, and familial amyotrophic lateral
XX sclerosis (FALS)), cardiovascular disease (e.g. atherosclerosis,
XX myocardial infarction, heart failure, cardiomyopathy, immune disease (e.g.
XX reperfusion injury, and hypertensive heart disease), insulin-dependent,
XX rheumatoid arthritis, systemic lupus erythematosus), cancer (e.g.
XX diabetes mellitus, lupus, pernicious anaemia, dermatomyositis, enythema
XX nodosum, Sjogren's syndrome, temporal arthritis, myasthenia gravis,
XX Wegener's granulomatosis, glomerulonephritis, anti-phospholipid syndrome,
XX and autoimmune polyarthritides), a neoplastic disorder (e.g. leukemia,
XX sarcomas, myelomas, carcinomas, neuromas, melanoma, cancers of the
XX breast, brain, colon, cervix, and prostate, Hodgkin's disease and
XX non-Hodgkin's lymphoma), inflammatory disorders (e.g. inflammatory joint
XX disorders and inflammatory induced cell damage to the eye, brain and
XX other organs), ischemia or reperfusion injury (e.g. myocardial ischemia
XX and reperfusion injury, renal ischemia, spinal cord ischemia and/or
XX reperfusion injury, retinal ischemia or infarction, and stroke), toxic
XX insult (e.g. liver toxicity, pulmonary toxicity, toxic damage to other
XX organs from chemicals, radiation, and other noxious substances), macular
XX degeneration, cataract formation, pancreatitis, Crohn's disease,
XX ulcerative colitis, accelerated aging, spinal cord disease (e.g. motor
XX neuron diseases, degeneration of the spinal cord, Guillan Bare Syndrome
XX and demyelinating disease), bypass surgery, chemotherapy,
XX chemically-induced reperfusion, and therapeutics such as clozapine, AZT,
XX and anthracyclines.
XX
XX Sequence 21 AA;
XX
XX Query Match 100.0%; Score 30; DB 20; Length 21;
XX Best Local Similarity 100.0%; Pred. No. 2.6;
XX Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 SVDVEY 6
XX DB 1 SVDVEY 6

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RESULT 9  
 ABB80007  
 ID ABB80007 standard; peptide; 21 AA.  
 XX AC  
 XX AC ABB80007;  
 XX DT 26-JUL-2002 (first entry)  
 XX DE Streptokinase derived peptide#7.  
 XX KW Streptokinase; cell death; apoptosis; necrosis; neurotropic;  
 KW neuroprotective; antiparkinsonian; anticonvulsant; cytostatic;  
 KW antiinflammatory; antithrombotic; antirheumatic; cardiac;  
 KW antiatherosclerotic; vasotropic; immunosuppressive; anti-HIV;  
 KW dermatological; antidiabetic; antinaemic; virucide; ophthalmological;  
 KW antitumor; antibacterial; antiparasitic; neurodegenerative disease;  
 KW Parkinson's disease; Alzheimer's disease; Huntington's disease;  
 KW cerebellar degeneration; neoplastic disorder; cancer;  
 KW inflammatory disorder; arthritis; inflammatory joint disorders;  
 KW cardiovascular disease; heart failure; atherosclerosis;  
 KW myocardial reperfusion injury; immune disease; autoimmune disease;  
 KW acquired immunodeficiency syndrome; AIDS; rheumatoid arthritis;  
 KW systemic lupus erythematosus; diabetes mellitus; pernicious anaemia;  
 KW myelodegenerative diseases; viral diseases; macular degeneration;  
 KW cataract; Crohn's disease; ulcerative colitis; pancreatitis;  
 KW prion disease; aging.  
 XX OS Synthetic.  
 XX PN US6348567-B1.  
 XX PD 19-FEB-2002.  
 XX PF 19-APR-1999; 99US-0294457.  
 XX PR 06-DEC-1995; 95US-008233P.  
 XX PR 05-DEC-1996; 96US-0759399.  
 XX (MOLE-) MOLECULAR THERAPEUTICS INC.  
 XX PA Krystal G, Rabkin SW;  
 XX PI WPI; 2002-266542/31.  
 XX DR New peptides obtained from streptokinase, useful in ameliorating cell  
 PT death due to apoptosis and/or necrosis and treating neurodegenerative,  
 PT neoplastic, immune, cardiovascular and inflammatory disorders -  
 XX Claim 9; Column 5; 18pp; English.  
 XX The invention relates to an isolated peptide obtained from streptokinase,  
 CC or its derivative or analog, which ameliorate cell death. The activity of  
 CC peptides of the invention may be described as, neurotropic,  
 CC neuroprotective, antiparkinsonian, anticonvulsant, cytostatic,  
 CC antiinflammatory, antithrombotic, antirheumatic, cardiac,  
 CC antiatherosclerotic, vasotropic, immunosuppressive, anti-HIV,  
 CC dermatological, antidiabetic, antinaemic, virucide, ophthalmological,  
 CC antitumor, antibacterial and antiparasitic. Peptides of the invention  
 CC ameliorates apoptosis and necrosis in a warm-blooded animal. Compositions  
 CC comprising peptides of the invention are useful for treating  
 CC neurodegenerative diseases (e.g. Parkinson's, Alzheimer's, Huntington's  
 CC disease and cerebellar degeneration) neoplastic disorders including  
 CC cancer, inflammatory disorders (e.g. arthritis, inflammatory joint  
 CC disorders), cardiovascular diseases (e.g. heart failure, atherosclerosis  
 CC and myocardial reperfusion injury), immune diseases (e.g. autoimmune  
 CC disease, acquired immunodeficiency syndrome (AIDS), rheumatoid arthritis,  
 CC systemic lupus erythematosus, diabetes mellitus, pernicious anaemia),  
 CC myelodegenerative diseases, viral diseases, and degenerative diseases of  
 CC any organ. Other disorders include macular degeneration, cataracts,  
 CC Crohn's disease, ulcerative colitis, cataracts, pancreatitis, infectious  
 CC diseases including bacteria, parasite, prion-based diseases, and

CC accelerated aging. The current sequence represents a streptokinase  
 CC derived peptide of the invention with an ability to ameliorate cell  
 CC death in cardiac myocytes.  
 XX SQ Sequence 21 AA;  
 Query Match 100.0%; Score 30; DB 23; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 2.6;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SVDVEY 6  
 DB 1 SVDVEY 6  
 RESULT 10  
 AAY01550  
 ID AAY01550 standard; peptide; 71 AA.  
 XX AC AAY01550;  
 XX DT 18-JUN-1999 (first entry)  
 XX DE Antigenic epitope of streptokinase, spanning amino acids 138-208.  
 KW Antigenic peptide; streptokinase; streptokinase-specific antibody;  
 KW thrombolytic activity; thrombolytic therapy; glomerulonephritis;  
 KW rheumatic fever.  
 XX OS Streptococcus equisimilis.  
 XX PN WO9908698-A1.  
 XX PD 25-FEB-1999.  
 XX PF 18-AUG-1998; 98WO-US17114.  
 XX PR 18-AUG-1997; 97US-0055911.  
 XX PA (GERO ) GEN HOSPITAL CORP.  
 XX PA (HARD ) HARVARD COLLEGE.  
 XX PI Parhami-Seren B, Reed GL;  
 XX WPI; 1999-190113/16.  
 XX New polypeptides which bind streptokinase-specific antibodies -  
 PT useful in thrombolytic therapy  
 XX Claim 16; Page 5; 44pp; English.  
 XX The present sequence represents an antigenic epitope of  
 CC streptokinase. The specification describes a polypeptide  
 CC which binds to a streptokinase-specific antibody and prevents the  
 CC antibody binding to native streptokinase. The specification also  
 CC describes a synthetic polypeptide (PI) comprising an epitope which  
 CC binds to a streptokinase-specific antibody and reduces thrombolytic  
 CC activity of streptokinase. PI is used in thrombolytic therapy, and to  
 CC prevent or treat glomerulonephritis and rheumatic fever.  
 XX SQ Sequence 71 AA;  
 Query Match 100.0%; Score 30; DB 20; Length 71;  
 Best Local Similarity 100.0%; Pred. No. 10;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SVDVEY 6  
 DB 20 SVDVEY 25  
 RESULT 11  
 AAY01558



ID AAY01558 standard; peptide; 146 AA.  
XX  
AC AAY01558;  
XX  
DT 18-JUN-1999 (first entry)  
XX  
DE Peptide corresponding to amino acids 148-293 of streptokinase.  
XX  
DE Antigenic peptide; streptokinase; streptokinase-specific antibody;  
KW thrombolytic activity; thrombolytic therapy; glomerulonephritis;  
KW rheumatic fever.  
KW  
XX Streptococcus equisimilis.  
OS  
XX WO9908698-A1.  
PN  
XX  
PD 25-FEB-1999.  
XX  
XX 18-AUG-1998; 98WO-US17114.  
XX  
PR 18-AUG-1997; 97US-0055911.  
XX  
XX (GEO ) GEN HOSPITAL CORP.  
PA (HARD ) HARVARD COLLEGE.  
PA  
XX Parhami-Seren B, Reed GL;  
PI WPI; 1999-190113/16.  
XX  
XX New polypeptides which bind streptokinase-specific antibodies -  
PT useful in thrombolytic therapy  
PT  
XX Disclosure; Page 13; 44pp; English.  
XX  
XX The present sequence represents a peptide corresponding to  
CC amino acids 148-293 of streptokinase. The specification describes a  
CC polypeptide which binds to a streptokinase-specific antibody and  
CC prevents the antibody binding to native streptokinase. The specification  
CC also describes a synthetic polypeptide (P1) comprising an epitope which  
CC binds to an streptokinase-specific antibody and reduces thrombolytic  
CC activity of streptokinase. P1 is used in thrombolytic therapy, and to  
CC prevent or treat glomerulonephritis and rheumatic fever.  
XX  
XX  
SQ Sequence 146 AA;  
Query Match 100.0%; Score 30; DB 20; Length 146;  
Best Local Similarity 100.0%; Pred. No. 23;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SVDVEY 6  
DB 10 SVDVEY 15  
RESULT 12  
AAY24796  
ID AAY24796 standard; Protein; 150 AA.  
XX  
XX AAY24796;  
AC  
XX 26-AUG-1999 (first entry)  
DT  
XX  
XX Recombinant streptokinase rSK144-293.  
DE  
XX Streptococcus; streptokinase; fibrin-dependent plasminogen activator;  
KW rSK; bacterial; blood clot; thrombotic condition;  
KW myocardial infarction; venous thrombosis; pulmonary embolism;  
KW cerebral thrombosis; graft thrombosis; arterial thrombosis.  
XX  
XX Streptococcus equisimilis.  
OS Synthetic.  
XX  
XX WO9931247-A1.  
PN

XX 24-JUN-1999.  
PD  
XX 15-DEC-1998; 98WO-US26694.  
PF  
XX 15-DEC-1997; 97US-0069497.  
PR  
XX (HARD ) HARVARD COLLEGE.  
PA  
XX Reed GL;  
PI WPI; 1999-395183/33.  
DR N-PSDB; AAX80494.  
DR  
XX N-terminally deleted streptokinase  
PT  
XX Claim 34; Page 67-68; 73pp; English.  
XX  
XX The present invention describes an isolated bacterial protein that  
CC induces fibrin-dependent plasminogen activation in a pharmaceutical  
CC composition for dissolving blood clots. Also described are: (1) a  
CC composition comprising an isolated modified streptokinase, the  
CC modification being removal of amino acid residues in the amino terminus;  
CC (2) a method for dissolving a blood clot in a subject, comprising  
CC administering to the subject a fibrin-dependent bacterial streptokinase; (3) an  
CC nucleic acid (1) encoding a modified bacterial streptokinase; the  
CC expression vector comprising (1); and (4) a host cell transformed with  
CC the expression vector of (3). The pharmaceutical composition comprising  
CC a bacterial fibrin-dependent plasminogen activator is useful for  
CC dissolving blood clots in patients with a thrombotic condition, e.g.  
CC myocardial infarction, venous thrombosis, pulmonary embolism, cerebral  
CC thrombosis, graft thrombosis and arterial thrombosis. The modified  
CC streptokinase can also be used in non-human mammals. Streptokinase  
CC activation of plasminogen is at least 10-fold, preferably 100-fold  
CC greater in the presence of fibrin than in the absence of fibrin. The  
CC modified streptokinase has at least one amino acid substitution that  
CC inactivates a substrate site for proteolytic cleavage. This reduces the  
CC rate of degradation of the streptokinase at least two-fold. The present  
CC sequence represents recombinant streptokinase, designated rSK144-293.  
XX  
SQ Sequence 150 AA;  
Query Match 100.0%; Score 30; DB 20; Length 150;  
Best Local Similarity 100.0%; Pred. No. 24;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SVDVEY 6  
DB 14 SVDVEY 19  
RESULT 13  
AAY01557  
ID AAY01557 standard; peptide; 233 AA.  
XX  
XX AAY01557;  
AC  
XX 18-JUN-1999 (first entry)  
DT  
XX  
XX Peptide corresponding to amino acids 120-352 of streptokinase.  
DE  
XX Antigenic peptide; streptokinase; streptokinase-specific antibody;  
KW thrombolytic activity; thrombolytic therapy; glomerulonephritis;  
KW rheumatic fever.  
XX  
XX Streptococcus equisimilis.  
OS  
XX WO9908698-A1.  
PN  
XX 25-FEB-1999.  
PD  
XX 18-AUG-1998; 98WO-US17114.  
PF  
XX



PR 18-AUG-1997; 97US-0055911.  
XX (GCHO ) GEN HOSPITAL CORP.  
PA (HARD ) HARVARD COLLEGE.  
XX Parhami-Seren B, Reed GL;  
XX WPI; 1999-190113/16.  
XX New polypeptides which bind streptokinase-specific antibodies -  
PT useful in thrombolytic therapy  
XX Disclosure; Page 13; 44pp; English.  
XX The present sequence represents a peptide corresponding to  
CC amino acids 120-352 of streptokinase. The specification describes a  
CC polypeptide which binds to a streptokinase-specific antibody and  
CC prevents the antibody binding to native streptokinase. The specification  
CC also describes a synthetic polypeptide (PI) comprising an epitope which  
CC binds to an streptokinase-specific antibody and reduces thrombolytic  
CC activity of streptokinase. PI is used in thrombolytic therapy, and to  
CC prevent or treat glomerulonephritis and rheumatic fever.  
XX  
XX Sequence 233 AA;  
SQ  
Query Match 100.0%; Score 30; DB 20; Length 233;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SVDVEY 6  
Db 38 SVDVEY 43  
RESULT 14  
AAR91599  
ID AAR91599 standard; Protein; 297 AA.  
XX AAR91599;  
XX AC  
XX 08-AUG-1996 (first entry)  
XX Streptokinase from pST-1.  
XX streptokinase; recombinant production; haemolytic Streptococcus.  
XX Synthetic.  
XX W09527050-A1.  
XX 12-OCT-1995.  
XX 03-APR-1995; 95WO-CN00024.  
XX 04-APR-1994; 94CN-0112106.  
XX (UYSH-) UNIV SHANGHAI MEDICAL.  
XX Song H;  
XX WPI; 1995-358628/46.  
XX N-PSDB; AAT29961.  
XX Prepn. of streptokinase - useful for treating thrombus diseases.  
XX Example 2; Page 6-8; 24pp; Chinese.  
XX The present sequence is that of streptokinase encoded by a pST-1  
CC HindIII fragment. Recombinant streptokinase can be produced by  
CC culturing bacteria transformed with a high efficiency plasmid contg.  
CC the streptokinase gene, amplified by using haemolytic Streptococcus  
CC as the template and using inducers based on the streptokinase nucleotide  
CC sequence. The recombinant streptokinase is used to treat thrombotic

CC diseases.  
XX  
SQ Sequence 297 AA;  
Query Match 100.0%; Score 30; DB 16; Length 297;  
Best Local Similarity 100.0%; Pred. No. 52;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SVDVEY 6  
Db 183 SVDVEY 188  
RESULT 15  
AAR10196  
ID AAR10196 standard; Protein; 348 AA.  
XX AAR10196;  
XX AC AAR10196;  
XX DT 28-MAR-1991 (first entry)  
XX Streptokinase (1-372, 45-68 deficient).  
XX streptokinase; thrombolytic agent; myocardial infarction.  
XX Synthetic.  
XX EP407942-A.  
XX 16-JAN-1991.  
XX 09-JUL-1990; 90EP-0113099.  
XX 11-APR-1990; 90JP-0096830.  
XX 11-JUL-1989; 89JP-0179432.  
XX 27-NOV-1989; 89JP-0307957.  
XX (SAKA ) OTSUKA PHARM FACTOR.  
XX Majima E, Ogino K, Ono K, Sakata Y, Uenoyama T;  
XX WPI; 1991-016179/03.  
XX Synthetic gene encoding streptokinase - scale, high purity prodn.  
XX of streptokinase used as a thrombolytic agent  
XX Claim 7; Page 59; 76pp; English.  
XX Streptokinase derivative having a C-terminal deletion (i.e. Pro  
CC 373-Lys 414) and Arg 45 to Gly 68 also being deleted. Derivatives  
CC show a decreased antigenicity, higher stability in blood and greater  
CC selectivity of thrombolytic activity and specificity.  
CC The protein is used as a thrombolytic agent in  
CC patients with lung thrombus or myocardial infarction.  
CC See also AAQ10230, AAR10195 and AAR10197-R10200.  
XX  
SQ Sequence 348 AA;  
Query Match 100.0%; Score 30; DB 12; Length 348;  
Best Local Similarity 100.0%; Pred. No. 63;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SVDVEY 6  
Db 133 SVDVEY 138  
RESULT 16  
AAY24795  
ID AAY24795 standard; Protein; 356 AA.  
XX AAY24795;  
XX

DE 26-AUG-1999 (first entry)  
XX Recombinant streptokinase rSK59-414.  
KW Streptococcus, streptokinase; fibrin-dependent plasminogen activator;  
XX nSK; rSK; bacterial; blood clot; thrombotic condition;  
XX myocardial infarction; venous thrombosis; pulmonary embolism;  
XX cerebral thrombosis; graft thrombosis; arterial thrombosis.  
XX Streptococcus equisimilis.  
OS Synthetic.  
XX WO9931247-A1.  
XX 24-JUN-1999.  
XX 15-DEC-1998; 98WO-US26694.  
XX 15-DEC-1997; 97US-0069497.  
XX (HARD ) HARVARD COLLEGE.  
XX Reed GL;  
XX WPI; 1999-395183/33.  
XX N-PSDB; AAX80493.  
XX N-terminally deleted streptokinase  
PT Claim 35; Page 65-66; 73pp; English.  
XX The present invention describes an isolated bacterial protein that  
CC induces fibrin-dependent plasminogen activation in a pharmaceutical  
CC composition for dissolving blood clots. Also described are: (1) a  
CC composition comprising an isolated modified streptokinase, the  
CC modification being removal of amino acid residues in the amino terminus;  
CC (2) a method for dissolving a blood clot in a subject, comprising  
CC administering to the subject a fibrin-dependent streptokinase protein;  
CC a nucleic acid (1) encoding a modified bacterial streptokinase; (3) an  
CC expression vector comprising (1); and (4) a host cell transformed with  
CC the expression vector of (3). The pharmaceutical composition comprising  
CC a bacterial fibrin-dependent plasminogen activator is useful for  
CC dissolving blood clots in patients with a thrombotic condition, e.g.  
CC myocardial infarction, venous thrombosis, pulmonary embolism, cerebral  
CC thrombosis, graft thrombosis and arterial thrombosis. The modified  
CC streptokinase can also be used in non-human mammals. Streptokinase  
CC activation of plasminogen is at least 10-fold, preferably 100-fold  
CC greater in the presence of fibrin than in the absence of fibrin. The  
CC modified streptokinase has at least one amino acid substitution that  
CC inactivates a substrate site for proteolytic cleavage. This reduces the  
CC rate of degradation of the streptokinase at least two-fold. The present  
CC sequence represents recombinant streptokinase, designated rSK59-414.  
XX  
SQ Sequence 356 AA;  
Query Match 100.0%; Score 30; DB 20; Length 356;  
Best Local Similarity 100.0%; Pred. No. 64;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SVDVEY 6  
DB 99 SVDVEY 104  
RESULT 17  
AAR12892  
ID AAR12892 standard; Protein; 369 AA.  
XX AAR12892;  
XX AC AAR12892;  
XX 25-MAR-2003 (updated)  
DT 17-SEP-1991 (first entry)  
XX

DE Truncated Met streptokinase.  
XX Fusion protein; blood clotting; coagulation; fibrinolysis;  
KW antithrombotic; thrombolysis; streptokinase; thrombin.  
XX Streptococcus equisimilis ATCC 9542 or ATCC 10009.  
XX FH Key Location/Qualifiers  
FT Protein 2..369  
FT /label= core streptokinase  
FT /note= "AAs 16-383"  
XX WO9109125-A.  
XX 27-JUN-1991.  
XX 07-DEC-1990; 90WO-GB01911.  
XX 07-DEC-1990; 90WO-GB01911.  
XX 07-DEC-1989; 89GB-0027722.  
XX (BRBI-) BRITISH BIO-TECHNOLOGY LTD.  
XX Dawson KM, Hunter MG, Czaplewski LG;  
XX WPI; 1991-208151/28.  
XX N-PSDB; AAQ12159.  
XX Fusion protein cleavage by blood clotting enzyme - for prodn. of  
PT fractions having greater antithrombotic activity for therapy and  
PT prophylaxis.  
XX Disclosure; Page 88; 115pp; English.  
XX The sequence was deduced from DNA obt'd. from PCR amplified chromo-  
CC somal DNA from S. equisimilis (Lancefield's Gp C ) ATCC 10009 or  
CC ATCC 9642. The gene was truncated by 15 codons at the 3' ter-  
CC minal and engineered to add a Met codon prior to codon 16 of the  
CC streptokinase CDS. The construct was used to prepare expression  
CC vector pG608 for prodn. of the streptokinase core molecule.  
CC See also AAR12887-R12889, AAR12891-R12893, AAR12885 and AAR12522.  
CC (Updated on 25-MAR-2003 to correct PA field.)  
XX Sequence 369 AA;  
Query Match 100.0%; Score 30; DB 12; Length 369;  
Best Local Similarity 100.0%; Pred. No. 67;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SVDVEY 6  
DB 143 SVDVEY 148  
RESULT 18  
AAR10195  
ID AAR10195 standard; Protein; 371 AA.  
XX AAR10195;  
XX AC AAR10195;  
XX 28-MAR-1991 (first entry)  
XX Streptokinase (1-372, Phe 118 deleted).  
XX streptokinase; thrombolytic agent; myocardial infarction.  
XX Synthetic.  
XX EP407942-A.  
XX 16-JAN-1991.  
XX 09-JUL-1990; 90EP-0113099.  
PF

XX 11-APR-1990; 90JP-0096830.  
PR 11-JUL-1989; 89JP-0179432.  
PR 27-NOV-1989; 89JP-0307957.  
XX (SAKA ) OTSUKA PHARM FACTOR.  
XX  
XX Majima E, Ogino K, Ono K, Sakata Y, Uenoyama T;  
XX WPI; 1991-016179/03.  
XX Synthetic gene encoding streptokinase - scale, high purity prodn.  
PT of streptokinase used as a thrombolytic agent  
XX  
XX Claim 8; Page 59; 76pp; English.  
XX  
XX Streptokinase derivative having a C-terminal deletion (i.e. Pro  
CC 373-Lys 414) and Phe at position 118 being deleted. Alternatively,  
CC Phe 118 can be replaced with any other amino acid. Derivatives show  
CC a decreased antigenicity, higher stability in blood and greater  
CC selectivity of thrombolytic activity and specificity.  
CC The protein is used as a thrombolytic agent in  
CC patients with lung thrombus or myocardial infarction.  
CC See also AAQ10230 and AAR10196-R10200.  
XX  
XX Sequence 371 AA;  
SQ  
Query Match 100.0%; Score 30; DB 12; Length 371;  
Best Local Similarity 100.0%; Pred. No. 67;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SVDVEY 6  
DB 156 SVDVEY 161  
RESULT 19  
AAR10197  
ID AAR10197 standard; Protein; 372 AA.  
XX  
XX AAR10197;  
XX  
XX 28-MAR-1991 (first entry)  
DT  
DE Streptokinase (1-372, Gln 256, Gln 257).  
XX  
XX streptokinase; thrombolytic agent; myocardial infarction.  
XX  
XX Synthetic.  
XX  
XX EP407942-A.  
XX  
XX 16-JAN-1991.  
XX  
XX 09-JUL-1990; 90EP-0113099.  
XX  
XX 11-APR-1990; 90JP-0096830.  
XX  
XX 11-JUL-1989; 89JP-0179432.  
XX  
XX 27-NOV-1989; 89JP-0307957.  
XX (SAKA ) OTSUKA PHARM FACTOR.  
XX  
XX Majima E, Ogino K, Ono K, Sakata Y, Uenoyama T;  
XX WPI; 1991-016179/03.  
XX  
XX Synthetic gene encoding streptokinase - scale, high purity prodn.  
PT of streptokinase used as a thrombolytic agent  
XX  
XX Claim 9; Page 59; 76pp; English.  
XX  
XX Streptokinase derivative having a C-terminal deletion (i.e. Pro  
CC 373-Lys 414) and Gln being substituted for Lys at both positions

CC 256 and 257. Derivatives show a decreased antigenicity, higher  
CC stability in blood and greater selectivity of thrombolytic activity  
CC and specificity. The protein is used as a thrombolytic agent in  
CC patients with lung thrombus or myocardial infarction.  
CC See also AAQ10230, AAR10195-6 and AAR10198-R10200.  
XX  
XX Sequence 372 AA;  
SQ  
Query Match 100.0%; Score 30; DB 12; Length 372;  
Best Local Similarity 100.0%; Pred. No. 68;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SVDVEY 6  
DB 157 SVDVEY 162  
RESULT 20  
AAR10200  
ID AAR10200 standard; Protein; 372 AA.  
XX  
XX AAR10200;  
XX  
XX 28-MAR-1991 (first entry)  
DT  
DE Streptokinase (1-372) derivative.  
XX  
XX streptokinase; thrombolytic agent; myocardial infarction.  
XX  
XX Synthetic.  
XX  
XX EP407942-A.  
XX  
XX 16-JAN-1991.  
XX  
XX 09-JUL-1990; 90EP-0113099.  
XX  
XX 11-APR-1990; 90JP-0096830.  
XX  
XX 11-JUL-1989; 89JP-0179432.  
XX  
XX 27-NOV-1989; 89JP-0307957.  
XX (SAKA ) OTSUKA PHARM FACTOR.  
XX  
XX Majima E, Ogino K, Ono K, Sakata Y, Uenoyama T;  
XX WPI; 1991-016179/03.  
XX  
XX Synthetic gene encoding streptokinase - scale, high purity prodn.  
PT of streptokinase used as a thrombolytic agent  
XX  
XX Claim 6; Page 59; 76pp; English.  
XX  
XX Streptokinase derivative having a C-terminal deletion (i.e. Pro  
CC 373-Lys 414) and retaining streptokinase activity. One or more of  
CC the amino acids can be replaced by a different amino acid at the  
CC same position or it can be deleted. Alternatively, an extra residue  
CC can be inserted into the sequence. Derivatives show  
CC a decreased antigenicity, higher stability in blood and greater  
CC selectivity of thrombolytic activity and specificity.  
CC The protein is used as a thrombolytic agent in  
CC patients with lung thrombus or myocardial infarction.  
CC See also AAQ10230 and AAR10195-R10199.  
XX  
XX Sequence 372 AA;  
SQ  
Query Match 100.0%; Score 30; DB 12; Length 372;  
Best Local Similarity 100.0%; Pred. No. 68;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SVDVEY 6  
DB 157 SVDVEY 162



PI Seralena Menendez A;  
XX WPI; 2000-226041/20.  
DR N-PSDB; AA299252.  
XX  
PT Recombinant production of streptokinase mutants, useful as thrombolytic  
PT agents for treating myocardial infarction, that are truncated at the N-  
PT or C-terminus -  
XX  
PS Disclosure; Page 24-25; 54pp; English.  
XX  
XX The present sequence represents a mutant protein of the streptokinase  
CC SKC-2. Streptokinase forms a complex with plasminogen, activating its  
CC conversion to plasmin. The SKC-2 gene was modified to produce the  
CC mutant protein. The obtained mutants conserve their capacity for  
CC plasminogen activator complex formation, thus having reduced  
CC antigenicity. The mutants are derived from the 1-1119 gene fragment,  
CC and retain the thrombolytic activity of SKC-2 but, compared with the  
CC full-length protein, are less antigenic and retain activity better in  
CC presence of antibodies that neutralize activity of the complete  
CC protein. The mutants are thrombolytic agents which are useful for  
CC treating myocardial infarction, pulmonary thromboembolism, surgical  
CC complications and other forms of thrombosis.  
XX  
SQ Sequence 384 AA;  
Query Match 100.0%; Score 30; DB 21; Length 384;  
Best Local Similarity 100.0%; Pred. No. 70;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SVDVEY 6  
Db 157 SVDVEY 162  
|||||  
RESULT 24  
ID AAR10199  
XX AAR10199 standard; Protein; 391 AA.  
AC AAR10199;  
XX  
DT 28-MAR-1991 (first entry)  
XX  
DE Streptokinase (1-372, 45-68 deficient, Gln 256, Gln 257).  
XX streptokinase; thrombolytic agent; myocardial infarction.  
KW  
XX Synthetic.  
OS  
XX EP407942-A.  
PN  
XX 16-JAN-1991.  
PD  
XX 09-JUL-1990; 90EP-0113099.  
PF  
XX 11-APR-1990; 90JP-0096830.  
PR 11-JUL-1989; 83JP-0179432.  
PR 27-NOV-1989; 83JP-0307957.  
XX  
XX (SAKA) OTSUKA PHARM FACTOR.  
PA  
XX Majima E, Ogino K, Ono K, Sakata Y, Uenoyama T;  
PI WPI; 1991-016179/03.  
XX  
XX Synthetic gene encoding streptokinase - scale, high purity prodn.  
PT of streptokinase used as a thrombolytic agent  
PT  
PS Claim 11; Page 59; 76pp; English.  
XX  
XX Streptokinase derivative having a C-terminal deletion (i.e. Pro  
CC 373-Lys 414) and Arg 45 to Gly 68 also being deleted. In addition  
CC Gln residues replace Lys at positions 256 and 257. This is an

CC example of a streptokinase derivative which is a combination of two  
CC individually claimed modifications. Derivatives  
CC show a decreased antigenicity, higher stability in blood and greater  
CC selectivity of thrombolytic activity and specificity.  
CC The protein is used as a thrombolytic agent in  
CC patients with lung thrombus or myocardial infarction.  
CC See also AAQ10230, AAR10195-8 and AAR10200.  
XX  
SQ Sequence 391 AA;  
Query Match 100.0%; Score 30; DB 12; Length 391;  
Best Local Similarity 100.0%; Pred. No. 72;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SVDVEY 6  
Db 134 SVDVEY 139  
|||||  
RESULT 25  
ID AAY84004  
XX AAY84004 standard; Protein; 401 AA.  
AC AAY84004;  
XX  
DT 03-JUL-2000 (first entry)  
XX  
DE Amino acid sequence of a mutant streptokinase.  
XX  
KW Streptokinase; SKC-2; plasminogen; plasmin; antigenicity;  
KW plasminogen activator complex formation; thrombolytic;  
KW myocardial infarction; pulmonary thromboembolism; thrombosis.  
XX  
XX Synthetic.  
OS  
XX Streptococcus equisimilis.  
XX  
XX EP985729-A2.  
PN  
XX 15-MAR-2000.  
PD  
XX 13-AUG-1999; 99EP-0202639.  
PF  
XX 14-AUG-1998; 98CU-0000119.  
PR  
XX  
XX (INGG-) CENT ING GENETICA & BIOTECNOLOGIA.  
PA  
XX Torrens Madrazo IDC, Garcia Ojalvo A, De La Fuente Garcia JDJ;  
PI Seralena Menendez A;  
PI  
XX  
XX WPI; 2000-226041/20.  
DR  
XX Recombinant production of streptokinase mutants, useful as thrombolytic  
PT agents for treating myocardial infarction, that are truncated at the N-  
PT or C-terminus -  
XX  
PS Disclosure; Page 18-20; 54pp; English.  
XX  
XX The present sequence represents a mutant protein of the streptokinase  
CC SKC-2. Streptokinase forms a complex with plasminogen, activating its  
CC conversion to plasmin. The SKC-2 gene was modified to produce the  
CC mutant protein. The obtained mutants conserve their capacity for  
CC plasminogen activator complex formation, thus having reduced  
CC antigenicity. The mutants are derived from the 1-1119 gene fragment,  
CC and retain the thrombolytic activity of SKC-2 but, compared with the  
CC full-length protein, are less antigenic and retain activity better in  
CC presence of antibodies that neutralize activity of the complete  
CC protein. The mutants are thrombolytic agents which are useful for  
CC treating myocardial infarction, pulmonary thromboembolism, surgical  
CC complications and other forms of thrombosis.  
XX  
SQ Sequence 401 AA;  
Query Match 100.0%; Score 30; DB 21; Length 401;

Best Local Similarity 100.0%; Pred. No. 74;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVDVEY 6  
Db 144 SVDVEY 149

RESULT 26  
AAV25020  
ID AAY25020 standard; peptide; 413 AA.  
XX AAY25020;  
XX AAY25020;  
DT 23-AUG-1999 (first entry)  
XX Streptokinase fragment.  
XX Streptokinase; cell death; amelioration; treatment; disease; aging; AIDS;  
KW cellular differentiation; physical insult; trauma; anoxia; hyperthermia;  
KW hypothermia; brain; spinal cord; kidney; heart; lung; liver; skin; HIV;  
KW viral disorder; hepatitis; retroviral; infection; encephalitis; FALS;  
KW neurodegenerative disorder; Parkinson's disease; Alzheimer's disease;  
KW Huntington's disease; cerebellar degeneration; cardiovascular disease;  
KW familial amyotrophic lateral sclerosis; atherosclerosis; heart failure;  
KW infarction; heart disease; cardiomyopathy; hypertensive; myocardial;  
KW reperfusion injury; immune disease; rheumatoid arthritis; renal; retinal;  
KW systemic lupus erythematosus; insulin-dependent; diabetes mellitus;  
KW pernicious anaemia; dermatomyositis; enychnema nodosum; myasthenia gravis;  
KW Sjogren's syndrome; temporal arthritis; autoimmune polyarthritides;  
KW Wegener's granulomatosis; glomerulonephritis; anti-phospholipid syndrome;  
KW neoplastic disorder; leukemia; sarcoma; myeloma; carcinoma; neuroma;  
KW melanoma; cancer; breast; colon; cervix; prostate; Hodgkin's disease;  
KW non-Hodgkin's lymphoma; inflammatory disorder; stroke; ischemia;  
KW spinal cord; toxic insult; pulmonary; macular degeneration; cataract;  
KW pancreatitis; Crohn's disease; ulcerative colitis; motor neuron disease;  
KW Guillan Bare Syndrome; demyelinating disease; bypass surgery;  
KW chemotherapy; clozapine; AZT; anthracycline.  
XX Unidentified.  
XX US5917013-A.  
XX 29-JUN-1999.  
XX 05-DEC-1996; 96US-0759599.  
XX 06-DEC-1995; 95US-0008233.  
XX 05-DEC-1996; 96US-0759599.  
XX (RABK/) RABKIN S W.  
XX Kryptal G, Rabkin SW;  
XX WPI; 1999-394231/33.  
XX Peptides that ameliorate cell death useful for treating conditions  
PT associated with cellular differentiation  
XX Disclosure; Fig 3; 15pp; English.  
XX AAY25009-Y25019 are novel peptides derived from streptokinase that  
CC ameliorate cell death. The products of the invention and their encoding  
CC nucleic acids may be useful for treating diseases and conditions related  
CC to aging, cellular differentiation, physical insult (e.g. physical  
CC trauma, anoxia, hyperthermia, hypothermia, chemically induced damage,  
CC and trauma to the brain, spinal cord, kidney, heart, lungs, liver, skin  
CC and any other organ), viral disorders (e.g. hepatitis, retroviral  
CC infections, viral encephalitis, and AIDS/HIV), neurodegenerative  
CC disorders (e.g. Parkinson's disease, Alzheimer's disease, Huntington's  
CC disease, cerebellar degenerations, and familial amyotrophic lateral  
CC sclerosis (FALS)), cardiovascular disease (e.g. atherosclerosis,  
CC myocardial infarction, heart failure, cardiomyopathy, myocardial

reperfusion injury, and hypertensive heart disease), immune disease (e.g.  
CC rheumatoid arthritis, systemic lupus erythematosus, insulin-dependent,  
CC diabetes mellitus, lupus, pernicious anaemia, dermatomyositis, enychnema  
CC nodosum, Sjogren's syndrome, temporal arthritis, myasthenia gravis,  
CC Wegener's granulomatosis, glomerulonephritis, anti-phospholipid syndrome,  
CC and autoimmune polyarthritides), a neoplastic disorder (e.g. leukemia,  
CC sarcomas, myelomas, carcinomas, neuromas, melanoma, cancers of the  
CC breast, brain, colon, cervix, and prostate, Hodgkin's disease and  
CC non-Hodgkin's lymphoma), inflammatory disorders (e.g. inflammatory joint  
CC disorders and inflammatory induced cell damage to the eye, brain and  
CC other organs), ischemia or reperfusion injury (e.g. myocardial ischemia  
CC and reperfusion injury, renal ischemia, spinal cord ischemia and/or  
CC reperfusion injury, retinal ischemia or infarction, and stroke), toxic  
CC insult (e.g. liver toxicity, pulmonary toxicity, toxic damage to other  
CC organs from chemicals, radiation, and other noxious substances), macular  
CC degeneration, cataract formation, pancreatitis, Crohn's disease,  
CC ulcerative colitis, accelerated aging, spinal cord disease (e.g. motor  
CC neuron diseases, degeneration of the spinal cord, Guillan Bare Syndrome  
CC chemically-induced reperfusion, and therapeutics such as clozapine, AZT,  
XX and anthracyclines.

SQ Sequence 413 AA;  
Query Match 100.0%; Score 30; DB 20; Length 413;  
Best Local Similarity 100.0%; Pred. No. 76;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVDVEY 6  
Db 156 SVDVEY 161

RESULT 27  
AAY84005  
ID AAY84005 standard; Protein; 413 AA.  
XX AAY84005;  
XX AAY84005;  
DT 03-JUL-2000 (first entry)  
XX Amino acid sequence of a mutant streptokinase.  
XX Streptokinase; SKC-2; plasminogen; plasmin; antigenicity;  
KW plasminogen activator complex formation; thrombolytic;  
KW myocardial infarction; pulmonary thromboembolism; thrombosis.  
XX Synthetic.  
XX Streptococcus equisimilis.  
XX EP985729-A2.  
XX 15-MAR-2000.  
XX 13-AUG-1999; 99EP-0202639.  
XX 14-AUG-1998; 98CU-0000119.  
XX (INGG-) CENT ING GENETICA & BIOTECNOLOGIA.  
XX Torrens Madrazo IDC, Garcia Ojalvo A, De La Fuente Garcia JDJ;  
PI Serailena Menendez A;  
XX WPI; 2000-226041/20.  
DR N-PSDB; AAZ99250.  
XX Recombinant production of streptokinase mutants, useful as thrombolytic  
PT agents for treating myocardial infarction, that are truncated at the N-  
XX or C-terminus  
PS Disclosure; Page 20-21; 54pp; English.  
XX The present sequence represents a mutant protein of the streptokinase

CC SKC-2. Streptokinase forms a complex with plasminogen, activating its  
CC conversion to plasmin. The SKC-2 gene was modified to produce the  
CC mutant protein. The obtained mutants conserve their capacity for  
CC plasminogen activator complex formation, thus having reduced  
CC antigenicity. The mutants are derived from the 1-1119 gene fragment,  
CC and retain the thrombolytic activity of SKC-2 but, compared with the  
CC full-length protein, are less antigenic and retain activity better in  
CC presence of antibodies that neutralize activity of the complete  
CC protein. The mutants are thrombolytic agents which are useful for  
CC treating myocardial infarction, pulmonary thromboembolism, surgical  
CC complications and other forms of thrombosis.

XX SQ Sequence 413 AA;  
Query Match 100.0%; Score 30; DB 21; Length 413;  
Best Local Similarity 100.0%; Pred. No. 76;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVDVEY 6  
Db 144 SVDVEY 149  
|||||

RESULT 28  
ID ABB80012 standard; protein; 413 AA.  
AC ABB80012;  
XX 26-JUL-2002 (first entry)  
XX Streptokinase amino acid sequence.

DE Streptokinase; cell death; apoptosis; necrosis; neurotropic;  
KW neuroprotective; antiparkinsonian; anticonvulsant; cytostatic;  
KW antiinflammatory; antiarthritic; antirheumatic; cardiant;  
KW antiatherosclerotic; vasotropic; immunosuppressive; anti-HIV;  
KW dermatological; antidiabetic; antianaemic; virucide; ophthalmological;  
KW antitumor; antibacterial; antiparasitic; neurodegenerative disease;  
KW Parkinson's disease; Alzheimer's disease; Huntington's disease;  
KW cerebellar degeneration; neoplastic disorder; cancer;  
KW inflammatory disorder; arthritis; inflammatory joint disorders;  
KW cardiovascular disease; heart failure; atherosclerosis;  
KW myocardial reperfusion injury; immune disease; autoimmune disease;  
KW acquired immunodeficiency syndrome; AIDS; rheumatoid arthritis;  
KW systemic lupus erythematosus; diabetes mellitus; pernicious anaemia;  
KW myelodegenerative diseases; viral diseases; macular degeneration;  
KW cataract; Crohn's disease; ulcerative colitis; pancreatitis;  
KW prion disease; aging.

OS Synthetic.  
XX US6348567-B1.  
XX 19-FEB-2002.  
XX 19-APR-1999; 99US-0294457.  
XX 06-DEC-1995; 95US-008233P.  
XX 05-DEC-1996; 96US-0759599.  
XX (MOLE-) MOLESCULAR THERAPEUTICS INC.  
XX Krystal G, Rabkin SW;  
XX WPI; 2002-266542/31.  
XX New peptides obtained from streptokinase, useful in ameliorating cell  
XX death due to apoptosis and/or necrosis and treating neurodegenerative,  
XX neoplastic, immune, cardiovascular and inflammatory disorders -  
XX Disclosure; Fig 3; 18pp; English.

CC The invention relates to an isolated peptide obtained from streptokinase,  
CC or its derivative or analog, which ameliorate cell death. The activity of  
CC peptides of the invention may be described as, neurotropic,  
CC neuroprotective, antiparkinsonian, anticonvulsant, cytostatic,  
CC antiinflammatory, antiarthritic, antirheumatic, cardiant,  
CC antiatherosclerotic, vasotropic, immunosuppressive, anti-HIV,  
CC dermatological, antidiabetic, antianaemic, virucide, ophthalmological,  
CC antitumor, antibacterial and antiparasitic. Peptides of the invention  
CC ameliorates apoptosis and necrosis in a warm-blooded animal. Compositions  
CC comprising peptides of the invention are useful for treating  
CC neurodegenerative diseases (e.g. Parkinson's, Alzheimer's, Huntington's  
CC disease and cerebellar degeneration) neoplastic disorders including  
CC cancer, inflammatory disorders (e.g. arthritis, inflammatory joint  
CC disorders), cardiovascular diseases (e.g. heart failure, atherosclerosis  
CC and myocardial reperfusion injury), immune diseases (e.g. autoimmune  
CC disease, acquired immunodeficiency syndrome (AIDS), rheumatoid arthritis,  
CC systemic lupus erythematosus, diabetes mellitus, pernicious anaemia),  
CC myelodegenerative diseases, viral diseases, and degenerative diseases of  
CC any organ. Other disorders include macular degeneration, cataracts,  
CC Crohn's disease, ulcerative colitis, cataracts, pancreatitis, infectious  
CC diseases including bacteria, parasite, prion-based diseases, and  
CC accelerated aging. The current sequence represents a representative  
CC streptokinase amino acid sequence.

XX SQ Sequence 413 AA;  
Query Match 100.0%; Score 30; DB 23; Length 413;  
Best Local Similarity 100.0%; Pred. No. 76;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVDVEY 6  
Db 156 SVDVEY 161  
|||||

RESULT 29  
ID ABG74199 standard; Protein; 413 AA.  
XX ABG74199;  
AC ABG74199;  
XX 06-MAY-2003 (first entry)  
XX Representative streptokinase sequence.

DE Cell death; streptokinase; neurodegenerative disorder; leukaemia; AIDS;  
KW Parkinson's disease; Alzheimer's disease; cardiovascular disease; trauma;  
KW atherosclerosis; myocardial infarction; immune disease; carcinoma;  
KW rheumatoid arthritis; neoplastic disorder; inflammatory disorder;  
KW arthritis; inflammatory induced cell damage; motor neuron disease;  
KW physical insult; severe shock; ischaemia; reperfusion injury; hepatitis;  
KW cell death associated procedure; spinal cord reperfusion injury;  
KW toxic insult; liver toxicity; pulmonary toxicity; spinal cord disease;  
KW Guillain-Barre syndrome; bypass surgery; myocardial ischaemia;  
KW chemotherapy; viral disease; viral encephalitis; infectious disease;  
KW bacterial disease; prion-based disease; macular degeneration;  
KW cataract formation; pancreatitis; Crohn's disease; ulcerative colitis;  
KW accelerated aging; oxidative stress.

OS Unidentified.  
XX 156..161  
XX /label= 6mer peptide #1  
XX /note= "Cell death ameliorating peptide. Specifically  
XX claimed in claim 2"

FT Key  
FT Peptide  
FT 156..171  
FT /label= 18mer peptide  
FT /note= "Cell death ameliorating peptide. Specifically  
FT claimed in claim 2. This is SEQ ID NO 5 as shown  
FT in the sequence listing"

FT Peptide  
FT 156..173  
FT /label= 18mer peptide





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XX PD 28-NOV-1991.
XX PF 31-MAY-1991; 91AU-0078101.
XX PR 23-MAY-1990; 90CU-0000090.
XX PA (INGG-) CENT ING GENETICA & BIOTECNOLOGIA.
XX PI Garcia MPE, Chaplen RR, Doce RS, Marrero LFH;
XX PI Collazo PR, Ramirez AC, Muncz EAM, Martinez WB, Sonavilla MC;
XX PI Fernandez AP, Garcia J, Martinez LSH;
XX DR WPI; 1992-024716/04.
XX DR N-PSDB; AAQ20665.
XX PT Streptokinase C-2 gene from S.equisimilis type C - plasmids and
XX PT transformants for large scale intra- and extracellular expression
XX PT of SKC-2 useful in thrombolytic agents
XX PS Claim 13; Page 14; 28pp; English.
XX CC The SKC-2 gene was isolated from S.equisimilis type C by gene
XX CC amplification from the synthetic primers SK1, SK2 and SK3 (see
XX CC AAQ20666-8). The SKC-2 gene was inserted into yeast expression vector
XX CC pBS-7 for extracellular expression of streptokinase and into pNAO
XX CC for intracellular expression in yeast. For expression in bacteria,
XX CC the SKC-2 gene was inserted in plasmid pBK3, between a trp promoter
XX CC and a T4 terminator.
XX CC (Updated on 25-MAR-2003 to correct PA field.)
XX SQ Sequence 414 AA;
XX Query Match 100.0%; Score 30; DB 13; Length 414;
XX Best Local Similarity 100.0%; Pred. No. 76;
XX Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVEY 6
Db 157 SVDVEY 162

RESULT 32
AAR63120
ID AAR63120 standard; protein; 414 AA.
XX AC AAR63120;
XX DT 25-MAR-2003 (updated)
XX DT 16-NOV-1994 (first entry)
XX DE Streptokinase.
XX KW Streptokinase; SK; Streptococcus equisimilis; plasminogen;
XX KW myocardial infarction.
XX OS Streptococcus equisimilis.
XX FH Key Location/Qualifiers
XX FT Region 14..414
XX FT /note= "claim 1, see CC"
XX FT Region 244..352
XX FT /note= "claim 2, see CC"
XX FT Region 1..352
XX FT /note= "claim 3, see CC"
XX FT Region 120..352
XX FT /note= "claim 3, see CC"
XX FT Region 244..414
XX FT /note= "claim 3, see CC"
XX WO9407992-A1.
XX PD 14-APR-1994.

XX PF 05-OCT-1993; 93WO-US09502.
XX PR 05-OCT-1992; 92US-0956692.
XX PR 29-SEP-1993; 93US-0128299.
XX PA (GEO ) GEN HOSPITAL CORP.
XX PA (HARD ) HARVARD COLLEGE.
XX PI Reed GL;
XX DR WPI; 1994-135561/16.
XX PT DNA encoding a polypeptide which binds to plasminogen and
XX PT corresponds to region of streptokinase - useful to detect
XX PT plasminogen in a sample and to treat myocardial infarction
XX PS Disclosure; Page 40-41; 62pp; English.
XX CC Nucleic acid comprising a sequence encoding amino acids
XX CC 14-414 of streptokinase, which binds to plasminogen and does
XX CC not have a sequence comprising amino acids 60-414 is new.
XX CC The polypeptide pref. comprises amino acids 244-352, 1-352,
XX CC 120-352 or 244-414.
XX CC (Updated on 25-MAR-2003 to correct PN field.)
XX SQ Sequence 414 AA;
XX Query Match 100.0%; Score 30; DB 15; Length 414;
XX Best Local Similarity 100.0%; Pred. No. 76;
XX Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVEY 6
Db 157 SVDVEY 162

RESULT 33
AAY24794
ID AAY24794 standard; Protein; 414 AA.
XX AC AAY24794;
XX DT 26-AUG-1999 (first entry)
XX DE Streptococcus equisimilis native streptokinase.
XX KW Streptococcus; streptokinase; fibrin-dependent plasminogen activator;
XX KW nSK; rSK; bacterial; blood clot; thrombotic condition;
XX KW myocardial infarction; venous thrombosis; pulmonary embolism;
XX KW cerebral thrombosis; graft thrombosis; arterial thrombosis.
XX OS Streptococcus equisimilis.
XX PN WO9931247-A1.
XX PD 24-JUN-1999.
XX PF 15-DEC-1998; 98WO-US26694.
XX PR 15-DEC-1997; 97US-0069497.
XX PA (HARD ) HARVARD COLLEGE.
XX PI Reed GL;
XX DR WPI; 1999-395183/33.
XX DR N-PSDB; AAX80492.
XX PT N-terminally deleted streptokinase
XX PS Claim 30; Page 60-61; 73pp; English.
XX XX
```

CC The present invention describes an isolated bacterial protein that  
CC induces fibrin-dependent plasminogen activation in a pharmaceutical  
CC composition for dissolving blood clots. Also described are: (1) a  
CC composition comprising an isolated modified streptokinase, the  
CC modification being removal of amino acid residues in the amino terminus;  
CC (2) a method for dissolving a blood clot in a subject, comprising  
CC administering to the subject a fibrin-dependent streptokinase protein;  
CC a nucleic acid (I) encoding a modified bacterial streptokinase protein;  
CC expression vector comprising (I); and (4) a host cell transformed with  
CC the expression vector of (3). The pharmaceutical composition comprising  
CC a bacterial fibrin-dependent plasminogen activator is useful for  
CC dissolving blood clots in patients with a thrombotic condition, e.g.  
CC myocardial infarction, venous thrombosis, pulmonary embolism, cerebral  
CC thrombosis, graft thrombosis and arterial thrombosis. The modified  
CC streptokinase can also be used in non-human mammals. Streptokinase  
CC activation of plasminogen is at least 10-fold, preferably 100-fold  
CC greater in the presence of fibrin than in the absence of fibrin. The  
CC modified streptokinase has at least one amino acid substitution that  
CC inactivates a substrate site for proteolytic cleavage. This reduces the  
CC rate of degradation of the streptokinase at least two-fold. The present  
CC sequence represents native streptokinase (nSK).  
XX  
SQ Sequence 414 AA;

Query Match 100.0%; Score 30; DB 20; Length 414;  
Best Local Similarity 100.0%; Pred. No. 76;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVEY 6  
Db 157 SVDVEY 162

RESULT 34  
AAAY01556  
ID AAY01556 standard; peptide; 414 AA.  
XX  
AC AAY01556;  
XX  
DT 18-JUN-1999 (first entry)  
XX  
DE Native streptokinase protein sequence.  
XX  
KW Antigenic peptide; streptokinase; streptokinase-specific antibody;  
KW thrombolytic activity; thrombolytic therapy; glomerulonephritis;  
KW rheumatic fever.  
XX  
OS Streptococcus equisimilis.  
XX  
PN WO9908698-A1.  
XX  
PD 25-FEB-1999.  
XX  
PF 18-AUG-1998; 98WO-US17114.  
XX  
PR 18-AUG-1997; 97US-0055911.  
XX  
PR (GEO ) GEN HOSPITAL CORP.  
PA (HARD ) HARVARD COLLEGE.  
XX  
PI Parhami-Seren B, Reed GL;  
XX  
DR WPI; 1999-190113/16.  
XX  
PT New polypeptides which bind streptokinase-specific antibodies -  
XX useful in thrombolytic therapy  
PS Disclosure; Page 12; 44pp; English.  
XX  
CC The present sequence represents a native streptokinase. The  
CC specification describes a polypeptide which binds to a  
CC streptokinase-specific antibody and prevents the antibody  
CC binding to native streptokinase. The specification also

CC describes a synthetic polypeptide (PI) comprising an epitope  
CC which binds to an streptokinase-specific antibody and reduces  
CC thrombolytic activity of streptokinase. PI is used in thrombolytic  
CC therapy, and to prevent or treat glomerulonephritis and rheumatic  
CC fever.  
XX  
SQ Sequence 414 AA;  
Query Match 100.0%; Score 30; DB 20; Length 414;  
Best Local Similarity 100.0%; Pred. No. 76;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVEY 6  
Db 157 SVDVEY 162

RESULT 35  
AAW94664  
ID AAW94664 standard; Protein; 414 AA.  
XX  
AC AAW94664;  
XX  
DT 04-MAY-1999 (first entry)  
XX  
DE Streptococcus equisimilis native streptokinase.  
XX  
KW Streptococcus equisimilis H46A; streptokinase; mutant; fibrinolytic;  
KW plasma clot; hydrolysis; haemolytic Streptococcus; plasminogen;  
KW plasmin; serine protease; fibrin; blood clot; thrombolytic;  
KW vascular thromboembolytic symptom; acute myocardial infarction;  
KW fibrinolysis; resistance.  
XX  
OS Streptococcus equisimilis.  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 14 /note= "encoded by ACC"  
XX  
PN US5876999-A.  
XX  
PD 02-MAR-1999.  
XX  
PF 06-DEC-1995; 95US-0568393.  
XX  
PR 06-DEC-1995; 95US-0568393.  
XX  
PA (NASC-) NAT SCI COUNCIL.  
XX  
PI Wu H;  
XX  
DR WPI; 1999-189643/16.  
DR N-PSDB; AAX16632.  
XX  
PT Mutant streptokinase polypeptide - useful as plasmin-resistant  
XX thrombolytic agent  
PS Claim 1; Column 7-10; 17pp; English.  
XX  
CC The present invention describes a mutant streptokinase (SK) polypeptide  
CC in which at least one of the amino acids in the Pro58-Lys59-Ser60-Lys61  
CC segment of the corresponding native SK is replaced by another amino acid.  
CC The present sequence represents native SK. SK is a secretory protein of  
CC haemolytic Streptococcus able to activate human plasminogen (Hplg) to  
CC plasmin (Hplm), which is a serine protease able to catalyse the  
CC hydrolysis of fibrin in blood clots. The SK is useful as a thrombolytic  
CC agent in the treatment of vascular thromboembolytic symptoms such as  
CC acute myocardial infarction. Compared with wild-type SK, the K59E mutant  
CC is more resistant to degradation by human plasmin and is more effective  
CC both in acting as a fibrinolytic agent and in activating human plasminogen.  
XX  
SQ Sequence 414 AA;

Query Match 100.0%; Score 30; DB 20; Length 414;  
Best Local Similarity 100.0%; Pred. No. 76;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVDVEY 6  
Db 157 SVDVEY 162

RESULT 36  
AAW94665  
ID AAW94665 standard; Protein; 414 AA.  
XX  
AC AAW94665;  
XX  
DT 04-MAY-1999 (first entry)  
XX  
DE Streptococcus equisimilis mutant streptokinase K59E.  
XX  
KW Streptococcus equisimilis H46A; streptokinase; mutant; fibrinolytic;  
KW plasma clot; hydrolysis; haemolytic Streptococcus; plasminogen;  
KW plasmin; serine protease; fibrin; blood clot; thrombolytic;  
KW vascular thromboembolytic symptom; acute myocardial infarction;  
KW fibrinolysis; resistance.  
XX  
OS Streptococcus equisimilis.  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 14 /note= "encoded by ACC"  
FT  
XX  
FN US5876999-A.  
XX  
XX  
PD 02-MAR-1999.  
XX  
PF 06-DEC-1995; 95US-0568393.  
XX  
XX 06-DEC-1995; 95US-0568393.  
XX  
PR (NASC-) NAT SCI COUNCIL.  
XX  
PA Wu H;  
XX  
PI WPI; 1999-189643/16.  
XX  
DR N-PSDB; AAX16633.  
XX  
XX  
PT Mutant streptokinase polypeptide - useful as plasmin-resistant  
PT thrombolytic agent  
XX  
PS Claim 4; Column 11-14; 17pp; English.  
XX  
CC The present invention describes a mutant streptokinase (SK) polypeptide  
CC in which at least one of the amino acids in the Pro58-Lys59-Ser60-Lys61  
CC segment of the corresponding native SK is replaced by another amino acid.  
CC The present sequence is mutant SK K59E. SK is a secretory protein of  
CC haemolytic Streptococcus able to activate human plasminogen (Hplg) to  
CC plasmin (Hplm), which is a serine protease able to catalyse the  
CC hydrolysis of fibrin in blood clots. The SK is useful as a thrombolytic  
CC agent in the treatment of vascular thromboembolytic symptoms such as  
CC acute myocardial infarction. Compared with wild-type SK, the K59E mutant  
CC is more resistant to degradation by human plasmin and is more effective  
CC both in acting as a fibrinolytic agent and in activating human plasminogen.  
XX  
SQ Sequence 414 AA;

Query Match 100.0%; Score 30; DB 20; Length 414;  
Best Local Similarity 100.0%; Pred. No. 76;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVDVEY 6  
Db 157 SVDVEY 162

RESULT 37  
AAW86143  
ID AAW86143 standard; Protein; 414 AA.  
XX  
AC AAW86143;  
XX  
DT 03-MAR-1999 (first entry)  
XX  
DE Streptokinase (SK) protein sequence.  
XX  
KW Non-immunogenic; epitope; T-cell; immunogenicity; immune system; SK;  
KW immunogl bulin; therapeutic; streptokinase.  
XX  
OS Streptococcus equisimilis.  
XX  
PN WO9852976-A1.  
XX  
PD 26-NOV-1998.  
XX  
PF 21-MAY-1998; 98WO-GB01473.  
XX  
PR 14-APR-1998; 98GB-0007751.  
PR 21-MAY-1997; 97GB-0010480.  
PR 31-JUL-1997; 97GB-0016197.  
PR 28-NOV-1997; 97GB-0025270.  
PR 02-DEC-1997; 97US-0067235.  
XX  
PA (BIOV-) BIOVATION LTD.  
XX  
PI Carr FU;  
XX  
DR WPI; 1999-045301/04.  
XX  
PT Reducing immunogenicity of proteins - by modifying the amino acid  
PT sequence of the protein to eliminate potential epitopes for T-cells  
PT of a given species  
XX  
PS Example 6; Fig 28; 77pp; English.  
XX

The invention relates to a method for the production of non-immunogenic proteins. The method comprises determining at least part of the amino acid sequence of the protein; (b) identifying in the amino acid sequence one or more potential epitopes for T-cells (T-cell epitopes) of the given species; and (c) modifying the amino acid sequence to eliminate at least one of the T-cell epitopes identified in step (b) thereby to eliminate or reduce the immunogenicity of the protein when exposed to the immune system of the given species. A method of analysing a pre-existing protein to predict the basis for immunogenic responses is also provided. The methods can be used particularly for reducing the immunogenicity of immunoglobulins or therapeutic proteins, e.g. streptokinase (SK). The products can be used for diagnosis and therapy. The present sequence represents the amino acid sequence of the SK protein.

Query Match 100.0%; Score 30; DB 20; Length 414;  
Best Local Similarity 100.0%; Pred. No. 76;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVDVEY 6  
Db 157 SVDVEY 162

RESULT 38  
AAW86144  
ID AAW86144 standard; Protein; 414 AA.  
XX  
AC AAW86144;  
XX  
DT 03-MAR-1999 (first entry)

XX DE De-immunised streptokinase (SK) protein sequence.  
 XX KW Non-immunogenic; epitope; T-cell; immunogenicity; immune system; SK;  
 XX KW immunogl bulin; therapeutic; streptokinase; de-immunised.  
 XX OS Streptococcus equisimilis.  
 XX PN WO9852976-A1.  
 XX PD 26-NOV-1998.  
 XX PF 21-MAY-1998; 98WO-GB01473.  
 XX PR 14-APR-1998; 98GB-0007751.  
 XX PR 21-MAY-1997; 97GB-0010480.  
 XX PR 31-JUL-1997; 97GB-0016197.  
 XX PR 28-NOV-1997; 97GB-0025270.  
 XX PR 02-DEC-1997; 97US-0067235.  
 XX PA (BIOV-) BIOVATION LTD.  
 XX PI Carr FJ;  
 XX PI WPI; 1999-045301/04.  
 XX DR Reducing immunogenicity of proteins - by modifying the amino acid  
 XX PT sequence of the protein to eliminate potential epitopes for T-cells  
 XX PT of a given species  
 XX PS Example 6; Fig 29; 77pp; English.  
 XX CC The invention relates to a method for the production of non-immunogenic  
 XX CC proteins. The method comprises determining at least part of the amino  
 XX CC acid sequence of the protein; (b) identifying in the amino acid sequence  
 XX CC one or more potential epitopes for T-cells (T-cell epitopes) of the given  
 XX CC species; and (c) modifying the amino acid sequence to eliminate at least  
 XX CC one of the T-cell epitopes identified in step (b) thereby to eliminate or  
 XX CC reduce the immunogenicity of the protein when exposed to the immune  
 XX CC system of the given species. A method of analysing a pre-existing protein  
 XX CC to predict the basis for immunogenic responses is also provided. The  
 XX CC methods can be used particularly for reducing the immunogenicity of  
 XX CC immunoglobulins or therapeutic proteins, e.g. Streptokinase (SK). The  
 XX CC products can be used for diagnosis and therapy. The present sequence  
 XX CC represents the amino acid sequence of a de-immunised SK protein molecule.  
 XX SQ Sequence 414 AA;  
 Query Match 100.0%; Score 30; DB 20; Length 414;  
 Best Local Similarity 100.0%; Pred. No. 76;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SVDVEY 6  
 Db 157 SVDVEY 162  
 RESULT 39  
 AAY90282  
 ID AAY90282 standard; Protein; 414 AA.  
 XX AC AAY90282;  
 XX DT 13-OCT-2000 (first entry)  
 XX DE S. equisimilis streptokinase.  
 XX KW Streptokinase; SK; hybrid plasminogen activator; fibrin binding region;  
 XX KW plasminogen; human; fibrinectin; thrombolytic therapy;  
 XX KW cardiovascular disorder; fibrinectin.  
 XX OS Streptococcus equisimilis.

PN EP1024192-A2.  
 XX PD 02-AUG-2000.  
 XX PF 23-DEC-1999; 99EP-0310541.  
 XX PR 24-DEC-1998; 98IN-0003825.  
 XX PA (COUL) CSIR COUNCIL SCI IND RES.  
 XX PI Sahni G, Kumar R, Roy C, Rajogopal K, Nihalani D, Sundaram V;  
 XX PI Yadav M;  
 XX DR WPI; 2000-516032/47.  
 XX DR N-PSDB; AAA37633.  
 XX PT Hybrid streptokinase-fibrin binding domain polypeptides useful for  
 XX PT thrombolytic therapy comprises a streptokinase fused with fibrin  
 XX PT binding domains of human fibrinectin -  
 XX PS Example 3; Fig 3; 58pp; English.  
 XX CC This sequence represents the human Streptococcus equisimilis  
 XX CC streptokinase protein sequence. The invention relates to a hybrid  
 XX CC plasminogen activator (PA) comprises a polypeptide fusion between  
 XX CC streptokinase (SK), which are capable of plasminogen (PG) activation,  
 XX CC and fibrin binding regions of human fibrinectin, which are from fibrin  
 XX CC binding domains (FBD) 4 and 5 or 1 and 2. The hybrid PA possesses the  
 XX CC ability to bind with fibrin independently and also characteristically  
 XX CC retains a PG activation ability which becomes evident only after a  
 XX CC pronounced duration, or lag, after exposure of the PA to a suitable  
 XX CC animal or human PG. The hybrid streptokinase-fibrin binding domain  
 XX CC polypeptides are useful in thrombolytic therapy for various kinds of  
 XX CC cardiovascular disorders. The hybrids have enhanced fibrin selectivity as  
 XX CC well as kinetics of plasminogen activation that are distinct from that of  
 XX CC natural streptokinase in being characterised by a temporary delay, or  
 XX CC lag of several minutes in the natural rate of the catalytic conversion  
 XX CC of plasminogen to plasmin (i.e. delayed-action thrombolysis). The  
 XX CC proteins can bind tightly with fibrin in blood clots soon after  
 XX CC introduction into the vascular system without significantly activating  
 XX CC the circulating blood plasminogen to plasmin, thus aiding in the  
 XX CC localisation of the plasminogen activation process to the site of  
 XX CC pathological thrombus. This overcomes systemic plasminogen activation  
 XX CC encountered during clinical use of streptokinase.  
 XX SQ Sequence 414 AA;  
 Query Match 100.0%; Score 30; DB 21; Length 414;  
 Best Local Similarity 100.0%; Pred. No. 76;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SVDVEY 6  
 Db 157 SVDVEY 162  
 RESULT 40  
 AAB01295  
 ID AAB01295 standard; protein; 414 AA.  
 XX AC AAB01295;  
 XX DT 25-SEP-2000 (first entry)  
 XX DE Wild type streptokinase from Streptococcus equisimilis.  
 XX KW Immunogenicity; immunogen; T cell epitope; T-lymphocyte; drug;  
 XX KW vaccine; carrier; diagnosis; therapy; complement; C3; C5; CVP;  
 XX KW plasminogen; streptokinase; fibrin; blood clot; thrombolysis;  
 XX KW plasmin; myocardial infarction.  
 XX OS Streptococcus equisimilis.

PN WO200034317-A2.  
XX 15-JUN-2000.  
XX 08-DEC-1999; 99WO-GB04119.  
XX 08-DEC-1998; 98GB-0026925.  
PR 02-FEB-1999; 99GB-0002139.  
XX (BIOV-) BIOVATION LTD.  
XX Carr FU, Adair FS, Hamilton AA, Carter G;  
XX WPI; 2000-423372/36.  
XX  
XX Rendering a protein non-immunogenic or less immunogenic useful in  
PT medicine and in diagnostics involves determining the amino acid  
PT sequence of the protein, identifying and modifying potential epitopes  
XX  
XX Example 2; Fig 5; 42pp; English.  
XX  
XX Proteins or their fragments can be rendered non-immunogenic or less  
CC immunogenic by identifying one or more potential T cell epitopes and  
CC modifying the sequence to eliminate at least one of these T cell  
CC epitopes to reduce the immunogenicity of the protein when exposed to  
CC the immune system of another organism. The method can be used for  
CC producing a protein with an enzymatic activity which has a beneficial  
CC therapeutic effect, a protein used to convert inactive drugs to its  
CC active form within a living organism, a vaccine, a protein used as a  
CC carrier of other molecule or a protein which binds to other molecules  
CC within or introduced within the living organism in order to alter the  
CC bio distribution of other molecules, such that the protein does not  
CC stimulate immune response in the living organism. The less immunogenic  
CC protein is useful in medicine, diagnosis and in manufacture of a  
CC therapeutic or a diagnostic agent. Streptokinase is produced by  
CC certain strains of beta-haemolytic streptococci. The protein has no  
CC inherent enzymatic activity but has considerable clinical importance  
CC potentiating its activation to plasmin and thereby promoting the  
CC dissolution of fibrin filaments in blood clots. Streptokinase is an  
CC effective thrombolytic agent in the treatment of coronary thrombosis,  
CC improving survival and preserving left ventricular function following  
CC myocardial infarction. The native protein is immunogenic and the  
CC production of neutralising antibodies in humans generally limits the  
CC protein to a single use. The new method could provide a longer  
CC therapeutic use for streptokinase. This is the sequence  
CC of the wild type streptokinase. The altered streptokinase sequence  
CC is given in AAB01296. See GENESSEQ records AAB01289-B01302.  
XX  
SQ Sequence 414 AA;  
Query Match 100.0%; Score 30; DB 21; Length 414;  
Best Local Similarity 100.0%; Pred. No. 76;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 SVDVEY 6  
Db 157 SVDVEY 162  
RESULT 41  
AAB01296  
ID AAB01296 standard; protein; 414 AA.  
XX  
XX AAB01296;  
AC  
XX 25-SEP-2000 (first entry)  
DT  
DE Altered streptokinase from Streptococcus equisimilis.  
XX  
XX Immunogenicity; immunogen; T cell epitope; T-lymphocyte; drug;  
KW vaccine; carrier; diagnosis; therapy; complement; C3; C5; C6;  
KW plasminogen; streptokinase; fibrin; blood clot; thrombolysis;

KW plasmin; myocardial infarction.  
XX Synthetic.  
OS Streptococcus equisimilis.  
XX  
PN WO200034317-A2.  
XX 15-JUN-2000.  
XX 08-DEC-1999; 99WO-GB04119.  
XX 08-DEC-1998; 98GB-0026925.  
PR 02-FEB-1999; 99GB-0002139.  
XX (BIOV-) BIOVATION LTD.  
XX Carr FU, Adair FS, Hamilton AA, Carter G;  
XX WPI; 2000-423372/36.  
XX  
XX Rendering a protein non-immunogenic or less immunogenic useful in  
PT medicine and in diagnostics involves determining the amino acid  
PT sequence of the protein, identifying and modifying potential epitopes  
XX  
XX Example 2; Fig 6; 42pp; English.  
XX  
XX Proteins or their fragments can be rendered non-immunogenic or less  
CC immunogenic by identifying one or more potential T cell epitopes and  
CC modifying the sequence to eliminate at least one of these T cell  
CC epitopes to reduce the immunogenicity of the protein when exposed to  
CC the immune system of another organism. The method can be used for  
CC producing a protein with an enzymatic activity which has a beneficial  
CC therapeutic effect, a protein used to convert inactive drugs to its  
CC active form within a living organism, a vaccine, a protein used as a  
CC carrier of other molecule or a protein which binds to other molecules  
CC within or introduced within the living organism in order to alter the  
CC bio distribution of other molecules, such that the protein does not  
CC stimulate immune response in the living organism. The less immunogenic  
CC protein is useful in medicine, diagnosis and in manufacture of a  
CC therapeutic or a diagnostic agent. Streptokinase is produced by  
CC certain strains of beta-haemolytic streptococci. The protein has no  
CC inherent enzymatic activity but has considerable clinical importance  
CC owing to its ability to efficiently bind human plasminogen,  
CC potentiating its activation to plasmin and thereby promoting the  
CC dissolution of fibrin filaments in blood clots. Streptokinase is an  
CC effective thrombolytic agent in the treatment of coronary thrombosis,  
CC improving survival and preserving left ventricular function following  
CC myocardial infarction. The native protein is immunogenic and the  
CC production of neutralising antibodies in humans generally limits the  
CC protein to a single use. The new method could provide a longer  
CC therapeutic use for streptokinase. This is the sequence  
CC of the wild type streptokinase. The altered streptokinase sequence  
CC is given in AAB01295. See GENESSEQ records AAB01289-B01302.  
XX  
SQ Sequence 414 AA;  
Query Match 100.0%; Score 30; DB 21; Length 414;  
Best Local Similarity 100.0%; Pred. No. 76;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 SVDVEY 6  
Db 157 SVDVEY 162  
RESULT 42  
AAB74940  
ID AAB74940 standard; protein; 414 AA.  
XX  
XX AAB74940;  
AC  
XX 02-JUL-2001 (first entry)  
DT  
XX

DE Mutant streptokinase protein sequence K59E.  
 XX Streptokinase; mutant; human; plasmin; plasminogen; thrombolytic.  
 XX Unidentified.

XX Key Location/Qualifiers  
 XX Misc-difference 59 /note= "Lys in wild type sequence"  
 XX Misc-difference 127 /label= unknown  
 XX Misc-difference 370 /note= "given as being encoded by NNN due to poor quality text"  
 XX /label= unknown  
 XX /note= "given as being encoded by NNN due to poor quality text"

XX TW416990-A.

XX 01-JAN-2001.

XX 11-JUL-1995; 95TW-0107238.

XX 11-JUL-1995; 95TW-0107238.

XX (NASC-) NAT SCI COUNCIL.

XX Wu H, Shr G;

XX WPI; 2001-326604/34.

XX N-PSDB; AAF92144.

XX Preparation of novel streptokinase mutants as improved thrombolytic agents -

XX Claim 1; Page 1; 4pp; Chinese.

XX The present invention describes a method to create mutants of streptokinase (SK) which become more resistant to hydrolytic inactivation by human plasmin (HPlm) and more effective in activation of human plasminogen (HPlg) than the native SK that is commercially available. The novel HPlm hydrolysis resistant SK can be created by the techniques of gene engineering to substitute the amino acid residues near the peptide bonds that are hydrolysed by HPlm. The mutant SK can be used to form HPlg and native SK and could be used as a thrombolytic agent. The mutant SK sequence could be coupled with other proteins to form fusion proteins and improve the fibrinolytic activity of the fusion proteins. Some truncated SKs such as SK(16-378) could activate HPlg as efficiently as native SK. The truncated SKs comprising the modification of Pro58-Lys59-Ser60-Lys61 to other amino acids would have a better thrombolytic activity than the corresponding native truncated SK. Since Lys59-Ser60 is among the few peptide bonds which are cleaved in the early reaction with HPlm and the NH2-terminal peptide chain of illel-Lys59 is essential in stabilising the structure of SK, the mutation at/or near by the peptide bond of Lys59-Ser60 should be able to prevent the hydrolysis of the peptide bond and might improve the stability of SK as a HPlg activator. The present sequence represents the mutant streptokinase (K59E) given in the present invention.  
 CC N.B. The present sequence corresponds to the indexers best interpretation of the sequence given in the specification, which is of poor quality print.

XX Sequence 414 AA;

Query Match 100.0%; Score 30; DB 22; Length 414;  
 Best Local Similarity 100.0%; Pred. No. 76;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVEY 6

DB 157 SVDVEY 162

RESULT 44

AA50870

ID AA50870 standard; protein; 415 AA.

XX AA50870;

RESULT 43

AA59593

ID AA59593 standard; protein; 415 AA.

XX AA59593;

XX 13-SEP-2000 (first entry)

XX Streptococcus plasminogen activator, streptokinase.

XX Plasminogen activator; cardiant; thrombolytic; heart attack; stroke; blood clotting disorder.

XX Streptococcus sp.

XX WO200032759-A1.

XX 08-JUN-2000.

XX 06-MAY-1999; 99WO-US09991.

XX 02-DEC-1998; 98US-0110588.

XX (OKLA-) OKLAHOMA MEDICAL RES FOUND.

XX Lin X, Zhang XC, Tang JUN;

XX WPI; 2000-422975/36.

XX Polypeptide with plasminogen activator activity useful as thrombolytic agent for treating blood clot disorders e.g. heart attack, comprises 10 amino acid peptide fragment for recognition or activation of plasminogen -

XX Disclosure; Page 29-31; 41pp; English.

XX The present sequence is streptokinase, a single-peptide secretory protein which is produced by various strains of haemolytic Streptococcus. Streptokinase forms a tight binding complex with human plasminogen, causing the spontaneous conversion of plasminogen to its active form, plasmin. Plasminogen is the principal serine protease zymogen in the extracellular fluids of vertebrates. Plasmin is implicated in pericellular proteolysis associated with a wide range of physiological and pathological processes. Plasminogen activators regulate plasminogen expression either by forming a binding complex, as in the case of streptokinase, or by hydrolysing a peptide bond in plasminogen to convert it to plasmin. Review of sequence homologies of several plasminogen activators and chymotrypsin has identified a six amino acid peptide involved in plasminogen activation. This peptide is particularly useful when inserted between amino acid residues 644 and 645 of full length human plasminogen. Novel plasminogen activators have been made based upon the plasminogen activation/recognition site of plasminogen binding proteins. The polypeptides are useful in preparing thrombolytic agents for treating blood clotting disorders such as heart attack.

XX Sequence 415 AA;

Query Match 100.0%; Score 30; DB 21; Length 415;

Best Local Similarity 100.0%; Pred. No. 77;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVEY 6

DB 157 SVDVEY 162

DT 24-FEB-2000 (first entry)  
XX Streptococcus sp. streptokinase protein fragment.  
DE Thrombolytic agent; streptokinase; antigenic; blood clot; heart attack;  
KW treatment.  
XX Homo sapiens.  
OS WO9957251-A2.  
PN 11-NOV-1999.  
PD 06-MAY-1999; 99WO-US10086.  
PF 06-MAY-1998; 98US-0084392.  
PR (OKLA-) OKLAHOMA MEDICAL RES FOUND.  
PA Zhang XC, Lin X, Tang JUN;  
XX WPI; 2000-052966/04.  
PI New thrombolytic agents derived from modified humanized streptokinase,  
XX useful for treating blood clot disorders -  
PT Example 5; Page 48-49; 55pp; English.  
XX This invention describes a novel thrombolytic agent comprising  
CC streptokinase where at least one nonessential portion has been modified.  
CC The invention also describes a method of forming a thrombolytic agent  
CC comprising determining a nonessential portion of streptokinase and  
CC modifying the nonessential portion to render the resulting protein less  
CC antigenic. The modified streptokinase is used to treat blood clot  
CC disorders, such as heart attacks. The modified streptokinase has less  
CC antigenicity than streptokinase but is still able to complex plasminogen  
CC and lead to plasminogen activation. Modified streptokinase with the  
CC nonessential portions removed or truncated simplify the molecule. Such  
CC smaller proteins are cheaper and easier to produce. This sequence  
CC represents a fragment of a Streptococcus sp. streptokinase protein  
CC which is used in the description of the method of the invention.  
XX  
SQ Sequence 415 AA;  
Query Match 100.0%; Score 30; DB 21; Length 415;  
Best Local Similarity 100.0%; Pred. No. 77;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SVDVEY 6  
Db 157 SVDVEY 162  
RESULT 45  
AAP50620  
ID AAP50620 standard; Protein; 440 AA.  
AC AAP50620;  
XX 16-OCT-1991 (first entry)  
DT Sequence encoded by skc streptokinase gene on the 2.5kb PstI  
DE produced pMFI fragment.  
XX Enzyme; thrombolytic agent; blood clot.  
KW Streptococcus equisimilis strain H46A (serological group C).  
XX AU6433859-A.  
PN 18-APR-1985.  
XX 05-OCT-1984; 84AU-0033859.  
PF

XX 02-MAR-1984; 84US-0585417.  
PR 10-OCT-1983; 83DD-025523.  
PR 10-OCT-1983; 83DD-0255235.  
XX (PHIP ) PHILLIPS PETROLEUM CO.  
PA (UYOR-) UNIV OF OKLAHOMA.  
XX Perretti JJ, Malke H;  
PI WPI; 1985-135032/23.  
DR N-PSDB; AAN50493.  
XX Streptokinase prodn. - by cultivating Escherichia coli ATCC 39613  
PT contg. recombinant plasmid pMFI  
XX Example; Fig 2; 28pp; English.  
XX Streptokinase produced using E.coli transformed with a recombinant  
CC streptokinase vector can be isolated for use as a thrombolytic agent  
CC to facilitate the in vivo lysis or dissolution of blood clots. The  
CC vector is esp. a plasmid obtd. from E.coli, esp. plasmid pBR 322.  
CC Recombinant plasmid pMFI as defined by a restriction endonuclease  
CC map is claimed. Escherichia coli HB 101 harbouring plasmid pMFI is  
CC deposited as ATCC 39613.  
XX  
SQ Sequence 440 AA;  
Query Match 100.0%; Score 30; DB 6; Length 440;  
Best Local Similarity 100.0%; Pred. No. 82;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SVDVEY 6  
Db 183 SVDVEY 188  
RESULT 46  
AAR06378  
ID AAR06378 standard; protein; 440 AA.  
XX AAR06378;  
AC AAR06378;  
XX 25-MAR-2003 (updated)  
DT 20-DEC-1990 (first entry)  
XX Streptokinase A from Streptococcus pyogenes SF130/13.  
DE Streptokinase A; recombinant phage; thrombolytic agent; plasminogen;  
KW plasmin.  
XX Streptococcus pyogenes.  
OS DD276694-A.  
XX DD276694-A.  
PN 07-MAR-1990.  
PD 07-NOV-1988; 88DD-0321532.  
PF 07-NOV-1988; 88DD-0321532.  
XX 07-NOV-1988; 88DD-0321532.  
PR (DEAK ) AKAD WISSENSCHAFTEN DDR.  
PA Walter F, Siegel M, Malke H;  
XX WPI; 1990-247328/33.  
DR N-PSDB; AAQ05604.  
XX High yield streptokinase A prodn. from infected bacteria - contg.  
PT recombinant phage including gene from Streptococcus, useful as  
XX thrombolytic agent  
PS Disclosure; Fig 2; 7pp; German.

XX Lambda L47.1 is ligated with genomic DNA from *S. pyogenes* SF130/13  
 CC and the resultant product used to transform bacteria. Infected  
 CC cells are cultured in liq. medium contg. assimilable C and N sources,  
 CC and streptokinase A is isolated from the cell lysate.  
 CC The infected cells provide the protein in high yields, i.e.  
 CC 1000 U/ml compared to 80 U/ml; for the donor strain.  
 CC The protein activates the autocatalytic conversion of human  
 CC plasminogen to human plasmin, so is potentially useful as a thrombolytic  
 CC agent. See also DD-276693 (AAQ05603).  
 CC (Updated on 25-MAR-2003 to correct PA field.)  
 XX

XX Sequence 440 AA;

Query Match 100.0%; Score 30; DB 11; Length 440;  
 Best Local Similarity 100.0%; Pred. No. 82;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVEY 6  
 Db 183 SVDVEY 188  
 |||||

RESULT 47  
 AAR06377  
 ID AAR06377 standard; protein; 440 AA.

XX

AC AAR06377;

XX 25-MAR-2003 (updated)

DT 20-DEC-1990 (first entry)

XX

XX Streptokinase G protein from *Streptococcus pyogenes* G19908.

XX

XX Streptokinase G; thrombolytic agent; plasminogen; plasmin;  
 KW recombinant plasmid.

XX

OS Streptococcus pyogenes.

XX

PN DD276693-A.

XX

PD 07-MAR-1990.

XX

PF 07-NOV-1988; 88DD-0321531.

XX

PR 07-NOV-1988; 88DD-0321531.

XX

XX (DEAK ) AKAD WISSENSCHAFTEN DDR.

XX

PI Walter F, Siegel M, Malke H;

XX

XX WPI; 1990-247327/33.

XX

DR N-PSDB; AAQ05603.

XX

PT High yield streptokinase G prodn. from recombinant cells -  
 PT transformed with plasmid contg. gene from *Streptococcus*, useful  
 PT as thrombolytic agent

XX

PS Disclosure; Fig 2; 7pp; German.

XX

XX Plasmid pW1 ( contg. the streptokinase G gene ) is ligated with  
 CC pUC19 and the resultant product used to transform bacteria. Infected  
 CC cells are cultured in liq. medium contg. assimilable C and N sources,  
 CC and streptokinase G is isolated from the cell lysate.  
 CC The infected cells provide the protein in high yields, i.e.  
 CC 600 U/ml which is 1.5-2 times that for the donor strain.

XX

XX The protein activates the autocatalytic conversion of human  
 CC plasminogen to human plasmin, so is potentially useful as a thrombolytic  
 CC agent. See also DD-276694 (AAQ05604).

XX

CC (Updated on 25-MAR-2003 to correct PA field.)

XX

SQ Sequence 440 AA;

Query Match 100.0%; Score 30; DB 12; Length 440;  
 Best Local Similarity 100.0%; Pred. No. 82;

Query Match 100.0%; Score 30; DB 11; Length 440;  
 Best Local Similarity 100.0%; Pred. No. 82;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVEY 6  
 Db 183 SVDVEY 188  
 |||||

RESULT 48

AAR12889  
 ID AAR12889 standard; protein; 440 AA.

XX

AC AAR12889;

XX

DT 25-MAR-2003 (updated)

DT 17-SEP-1991 (first entry)

XX

XX Streptokinase.

XX

XX Fusion protein; blood clotting; coagulation; fibrinolysis;  
 KW antithrombotic; thrombolysis; streptokinase.

XX

OS *Streptococcus equisimilis* ATCC 9542 or ATCC 100009.

XX

XX Key Location/Qualifiers

XX

FT Peptide 1..26

XX

FT Protein /label= signal sequence

XX

FT FT /label= mature streptokinase

XX

PN WO9109125-A.

XX

PD 27-JUN-1991.

XX

PF 07-DEC-1990; 90WO-GB01911.

XX

PR 07-DEC-1990; 90WO-GB01911.

XX

PR 07-DEC-1989; 89GB-0027722.

XX

PA (BRBI-) BRITISH BIO-TECHNOLOGY LTD.

XX

PI Dawson KM, Hunter MG, Czaplewski LG;

XX

XX WPI; 1991-208151/28.

XX

DR N-PSDB; AAQ12156.

XX

PT Fusion protein cleavage by blood clotting enzyme - for prodn. of  
 PT fractions having greater antithrombotic activity for therapy and  
 PT prophylaxis.

XX

PS Disclosure; Page 80; 115pp; English.

XX

XX The sequence was deduced from PCR amplified chromosomal DNA from  
 CC *S. equisimilis* (Lancefield's Gp C) ATCC 10009 or ATCC 9642. The  
 CC primers used for the PCR were based on the published DNA sequence  
 CC of *S. equisimilis* strain H46A (Malke, H., Roe, B., and Ferratti,  
 CC J.J., Gene 34 357-362 [1985]). See Swiss-Pat K02986 and P00779  
 CC and Geneseg N70106. The gene can be used to construct expression  
 CC vectors in which the streptokinase gene is linked to a second gene  
 CC encoding e.g. another streptokinase protein, hirudin, or a strepto-  
 CC kinase-like protein, via a linking sequence encoding a cleavage  
 CC site for e.g. factor Xa or thrombin. The enzymes which cleave the  
 CC fusion protein are present at the site of the target thrombus so  
 CC the active agents are released specifically at the place where clot  
 CC formation is occurring.  
 CC See also R12887, R12888, R12891-R12894, R12885 and R12522.  
 CC (Updated on 25-MAR-2003 to correct PA field.)  
 XX

SQ Sequence 440 AA;



Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVDVEY 6  
|||||

Db 183 SVDVEY 188

RESULT 49  
ABP29561  
ID ABP29561 standard; Protein; 440 AA.  
AC ABP29561;  
XX  
DT 02-JUL-2002 (first entry)  
DE Streptococcus polypeptide SEQ ID NO 8298.  
XX  
KW Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae;  
KW group A streptococcus; Streptococcus pyogenes; antibacterial;  
KW antiinflammatory; infection; vaccine; meningitis; gene therapy.  
XX  
OS Streptococcus pyogenes.  
XX  
PN WO200234771-A2.  
XX  
PD 02-MAY-2002.  
XX  
PF 29-OCT-2001; 2001WO-GB04789.  
XX  
PR 27-OCT-2000; 2000GB-0026333.  
PR 24-NOV-2000; 2000GB-0028727.  
PR 07-MAR-2001; 2001GB-0005640.  
XX  
PA (CHIR-) CHIRON SPA.  
PA (GENO-) INST GENOMIC RES.  
XX  
PI Telford J, Masignani V, Margarit Ros YI, Grandi G, Fraser C;  
PI Tettelin H;  
XX  
DR WPI; 2002-352536/38.  
DR N-PSDB; ABN70192.  
XX  
XX New Streptococcus protein for the treatment or prevention of infection  
or disease caused by Streptococcus bacteria, such as meningitis, and  
for detecting a compound that binds to the protein -  
PS Claim 1; Page 3946; 4525pp; English.  
XX  
XX The invention relates to a protein (ABP25413-ABP30895) from group B  
streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS  
(Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in  
the specification. The proteins have antibacterial and antiinflammatory  
activity. (I), nucleic acids encoding (I), ABN6044-ABN71526 and  
antibodies that bind (I) are used in the manufacture of medicaments for  
the treatment or prevention of infection or disease caused by  
Streptococcus bacteria, particularly S. agalactiae and S. pyogenes.  
Nucleic acids encoding (I) are used to detect Streptococcus in a  
biological sample. (I) is used to determine whether a compound binds to  
(I). A composition comprising (I) or a nucleic acid encoding (I), may be  
used as a vaccine or diagnostic composition. The disease caused by  
Streptococcus that is prevented or treated may be meningitis. Nucleic  
acid encoding (I) may be used to recombinantly produce (I) and may be  
used in gene therapy. Antibodies to (I) are used for affinity  
chromatography, immunoassays, and distinguishing/identifying  
Streptococcus proteins.  
XX  
SQ Sequence 440 AA;

Query Match 100.0%; Score 30; DB 23; Length 440;  
Best Local Similarity 100.0%; Pred. No. 82;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVDVEY 6

Db 183 SVDVEY 188

RESULT 50  
AAR12885  
ID AAR12885 standard; Protein; 483 AA.  
XX  
AC AAR12885;  
XX  
DT 25-MAR-2003 (updated)  
DT 17-SEP-1991 (first entry)  
XX  
DE Factor Xa-cleavable hirudin-IEGR-streptokinase.  
XX  
KW Fusion protein; blood clotting; coagulation; fibrinolysis;  
KW antithrombotic; thrombolysis.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FH 1..65 /label= hirudin HV-1  
FT Peptide 66..69  
FT /label= linker  
FT /note= "factor Xa cleavage site"  
FT Protein 70..483  
FT /label= streptokinase  
XX  
PN WO9109125-A.  
XX  
PD 27-JUN-1991.  
XX  
PF 07-DEC-1990; 90WO-GB01911.  
XX  
PR 07-DEC-1990; 90WO-GB01911.  
PR 07-DEC-1989; 89GB-0027722.  
XX  
PA (BRBI-) BRITISH BIO-TECHNOLOGY LTD.  
XX  
PI Dawson KM, Hunter MG, Czaplewski LG;  
XX  
DR WPI; 1991-208151/28.  
DR N-PSDB; AQA12162.  
XX  
XX Fusion protein cleavage by blood clotting enzyme - for prodr. of  
fractions having greater antithrombotic activity for therapy and  
prophylaxis.  
PT  
PT Disclosure; Page 96; 115pp; English.  
XX  
XX The protein is a recombinant product of a gene fusion construct.  
The sequence of the synthetic hirudin HV-1 genes was designed  
based on the published amino acid sequence (Dodd J., et al FEBS  
Letters 155 180 (1984)). The sequence of streptokinase was obd.  
from PCR amplified chromosomal DNA from S. equisimilis ATCC 10009  
or ATCC 9642. The primers used for the PCR were based on the pub-  
lished DNA sequence of S. equisimilis strain H46A (Malke, H., Roe,  
B., and Ferretti, J.J., Gene 34 357-362 [1985]). The two  
sequences were used to construct an expression vector in which the  
hirudin gene is linked to the streptokinase gene via a linking  
sequence encoding a cleavage site for factor Xa. The factor Xa is  
present at the site of the target thrombus so the active agents are  
released specifically at the place where clot formation is occurring.  
XX See also AAR12887-R12889, AAR12891-R12894 and AAR12522.  
XX (Updated on 25-MAR-2003 to correct PA field.)

SQ Sequence 483 AA;

Query Match 100.0%; Score 30; DB 12; Length 483;  
Best Local Similarity 100.0%; Pred. No. 91;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVDVEY 6  
| | | | |  
Db 226 SVDVEY 231

Search completed: January 20, 2004, 13:56:15  
Job time : 43 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 20, 2004, 13:56:57 ; Search time 33 Seconds

(without alignments)  
37.178 Million cell updates/sec

Title: US-09-919-703-1

Perfect score: 30

Sequence: 1 SDVEY 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 762491 seqs, 204481190 residues

Total number of hits satisfying chosen parameters: 762491

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 75 summaries

Database :

Published Applications AA:\*

- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*
- 6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep.\*
- 7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep.\*
- 8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*
- 9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pep.\*
- 10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep.\*
- 11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep.\*
- 12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep.\*
- 13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*
- 14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*
- 15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep.\*
- 16: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*
- 17: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*
- 18: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	30	100.0	6	10	US-09-919-703-1
2	30	100.0	16	10	US-09-919-703-5
3	30	100.0	20	10	US-09-919-703-6
4	30	100.0	21	10	US-09-919-703-7
5	30	100.0	413	10	US-09-919-703-12
6	30	100.0	414	11	US-09-940-235-2
7	30	100.0	414	12	US-10-300-215-252
8	30	100.0	414	12	US-10-300-215-253
9	30	100.0	891	10	US-09-862-027-25
10	29	96.7	1207	12	US-10-369-493-5723
11	28	93.3	629	12	US-10-369-493-6887
12	27	90.0	6	10	US-09-919-703-3
13	27	90.0	355	10	US-09-992-807-6
14	27	90.0	391	12	US-10-209-967-14
15	27	90.0	496	16	US-10-193-896-12

ALIGNMENTS

RESULT 1

US-09-919-703-1  
; Sequence 1, Application US/09919703  
; Patent No. US20020165129A1  
; GENERAL INFORMATION:  
; APPLICANT: Krysstal, Gerald  
; APPLICANT: Rabkin, Simon W.  
; TITLE OF INVENTION: Peptides and Their Use to Ameliorate

16	27	90.0	858	11	US-09-799-629-14	Sequence 14, Appl
17	27	90.0	858	11	US-09-927-315-25	Sequence 25, Appl
18	27	90.0	858	12	US-10-246-785-9	Sequence 9, Appl
19	27	90.0	858	12	US-10-190-417-25	Sequence 25, Appl
20	27	90.0	858	12	US-10-179-373-4	Sequence 4, Appl
21	27	90.0	858	15	US-10-035-045-14	Sequence 14, Appl
22	27	90.0	1471	12	US-10-369-493-1385	Sequence 1385, Ap
23	26	86.7	18	12	US-10-193-477-56	Sequence 56, Appl
24	26	86.7	282	9	US-09-737-149-43	Sequence 43, Appl
25	26	86.7	284	9	US-09-737-149-42	Sequence 42, Appl
26	26	86.7	285	9	US-09-737-149-12	Sequence 12, Appl
27	26	86.7	287	12	US-10-369-493-16538	Sequence 16538, A
28	26	86.7	305	12	US-10-369-493-22955	Sequence 22955, A
29	26	86.7	322	12	US-10-369-493-19042	Sequence 19042, A
30	26	86.7	349	15	US-10-156-761-12808	Sequence 12808, A
31	26	86.7	358	12	US-10-289-762-1049	Sequence 1049, Ap
32	26	86.7	395	12	US-10-369-493-1147	Sequence 1147, Ap
33	26	86.7	410	12	US-10-369-493-13245	Sequence 13245, A
34	26	86.7	461	10	US-09-738-626-5998	Sequence 5998, Ap
35	26	86.7	496	12	US-10-369-493-2914	Sequence 2914, Ap
36	26	86.7	496	16	US-10-193-896-11	Sequence 11, Appl
37	26	86.7	511	14	US-10-121-032-21	Sequence 21, Appl
38	26	86.7	511	15	US-10-093-037-21	Sequence 21, Appl
39	26	86.7	548	12	US-10-461-747-2	Sequence 2, Appl
40	26	86.7	572	9	US-09-815-242-13170	Sequence 13170, A
41	26	86.7	606	12	US-09-954-342-18	Sequence 18, Appl
42	26	86.7	606	12	US-09-954-342-20	Sequence 20, Appl
43	26	86.7	606	12	US-09-954-342-42	Sequence 42, Appl
44	26	86.7	606	12	US-10-193-477-4	Sequence 4, Appl
45	26	86.7	606	12	US-10-094-749-2513	Sequence 2513, Ap
46	26	86.7	694	15	US-10-128-714-3395	Sequence 3395, Ap
47	26	86.7	694	15	US-10-128-714-8395	Sequence 8395, Ap
48	26	86.7	725	12	US-10-369-493-4017	Sequence 4017, Ap
49	26	86.7	784	12	US-10-369-493-22944	Sequence 22944, A
50	26	86.7	968	12	US-10-291-265-281	Sequence 281, App
51	26	86.7	970	12	US-10-360-522-54	Sequence 54, Appl
52	26	86.7	972	12	US-10-360-522-61	Sequence 61, Appl
53	26	86.7	979	12	US-10-360-522-55	Sequence 55, Appl
54	26	86.7	979	12	US-10-360-522-58	Sequence 58, Appl
55	26	86.7	992	12	US-10-360-522-56	Sequence 56, Appl
56	26	86.7	1054	12	US-10-360-522-60	Sequence 60, Appl
57	26	86.7	1138	12	US-10-094-749-2576	Sequence 2576, Ap
58	26	86.7	1157	12	US-10-161-927-60	Sequence 60, Appl
59	26	86.7	1157	12	US-10-032-585-7459	Sequence 7459, Ap
60	26	86.7	1226	12	US-10-369-493-1078	Sequence 1078, Ap
61	25	83.3	172	12	US-10-104-047-2612	Sequence 2612, Ap
62	25	83.3	177	11	US-09-813-153-146	Sequence 146, App
63	25	83.3	238	12	US-10-369-493-18531	Sequence 18531, A
64	25	83.3	255	11	US-09-813-153-297	Sequence 297, App
65	25	83.3	329	12	US-10-369-493-19835	Sequence 19835, A
66	25	83.3	339	9	US-09-815-242-10953	Sequence 10953, A
67	25	83.3	349	12	US-10-166-225A-70	Sequence 70, Appl
68	25	83.3	353	12	US-10-369-493-14191	Sequence 14191, A
69	25	83.3	384	12	US-10-369-493-21430	Sequence 21430, A
70	25	83.3	419	12	US-10-369-493-5078	Sequence 5078, Ap
71	25	83.3	433	12	US-10-032-585-7006	Sequence 7006, Ap
72	25	83.3	449	12	US-10-369-493-14582	Sequence 14582, A
73	25	83.3	469	12	US-10-108-260A-4287	Sequence 4287, Ap
74	25	83.3	481	12	US-10-209-967-6	Sequence 6, Appl
75	25	83.3	593	12	US-10-369-493-14916	Sequence 14916, A

```
; TITLE OF INVENTION: Cell Death
; FILE REFERENCE: 50216/003004
; CURRENT APPLICATION NUMBER: US/09/919,703
; CURRENT FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: US 09/294,457
; PRIOR FILING DATE: 1999-04-19
; PRIOR APPLICATION NUMBER: US 08/759,599
; PRIOR FILING DATE: 1996-12-05
; PRIOR APPLICATION NUMBER: US 60/008,233
; PRIOR FILING DATE: 1995-12-06
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic polypeptide
US-09-919-703-1
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Query Match      100.0%; Score 30; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 SVDVEY 6
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Db       1 SVDVEY 6
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## RESULT 2

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US-09-919-703-5
; Sequence 5, Application US/09919703
; Patent No. US20020165129A1
; GENERAL INFORMATION:
; APPLICANT: Krystal, Gerald
; APPLICANT: Rabkin, Simon W.
; TITLE OF INVENTION: Peptides and Their Use to Ameliorate
; FILE REFERENCE: 50216/003004
; CURRENT APPLICATION NUMBER: US/09/919,703
; CURRENT FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: US 09/294,457
; PRIOR FILING DATE: 1999-04-19
; PRIOR APPLICATION NUMBER: US 08/759,599
; PRIOR FILING DATE: 1996-12-05
; PRIOR APPLICATION NUMBER: US 60/008,233
; PRIOR FILING DATE: 1995-12-06
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic polypeptide
US-09-919-703-5
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Query Match      100.0%; Score 30; DB 10; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 SVDVEY 6
        |||||
Db       1 SVDVEY 6
```

## RESULT 3

```
US-09-919-703-6
; Sequence 6, Application US/09919703
; Patent No. US20020165129A1
; GENERAL INFORMATION:
; APPLICANT: Krystal, Gerald
; APPLICANT: Rabkin, Simon W.
```

```
; TITLE OF INVENTION: Peptides and Their Use to Ameliorate
; TITLE OF INVENTION: Cell Death
; FILE REFERENCE: 50216/003004
; CURRENT APPLICATION NUMBER: US/09/919,703
; CURRENT FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: US 09/294,457
; PRIOR FILING DATE: 1999-04-19
; PRIOR APPLICATION NUMBER: US 08/759,599
; PRIOR FILING DATE: 1996-12-05
; PRIOR APPLICATION NUMBER: US 60/008,233
; PRIOR FILING DATE: 1995-12-06
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic polypeptide
US-09-919-703-6
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Query Match      100.0%; Score 30; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 SVDVEY 6
        |||||
Db       1 SVDVEY 6
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## RESULT 4

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US-09-919-703-7
; Sequence 7, Application US/09919703
; Patent No. US20020165129A1
; GENERAL INFORMATION:
; APPLICANT: Krystal, Gerald
; APPLICANT: Rabkin, Simon W.
; TITLE OF INVENTION: Peptides and Their Use to Ameliorate
; FILE REFERENCE: 50216/003004
; CURRENT APPLICATION NUMBER: US/09/919,703
; CURRENT FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: US 09/294,457
; PRIOR FILING DATE: 1999-04-19
; PRIOR APPLICATION NUMBER: US 08/759,599
; PRIOR FILING DATE: 1996-12-05
; PRIOR APPLICATION NUMBER: US 60/008,233
; PRIOR FILING DATE: 1995-12-06
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic polypeptide
US-09-919-703-7
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Query Match      100.0%; Score 30; DB 10; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 SVDVEY 6
        |||||
Db       1 SVDVEY 6
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## RESULT 5

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US-09-919-703-12
; Sequence 12, Application US/09919703
; Patent No. US20020165129A1
; GENERAL INFORMATION:
; APPLICANT: Krystal, Gerald
```

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; APPLICANT: Rabkin, Simon W.
; TITLE OF INVENTION: Peptides and Their Use to Ameliorate
; FILE REFERENCE: 50216/003004
; CURRENT APPLICATION NUMBER: US/09/919,703
; CURRENT FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: US 09/294,457
; PRIOR FILING DATE: 1999-04-19
; PRIOR APPLICATION NUMBER: US 08/759,599
; PRIOR FILING DATE: 1996-12-05
; PRIOR APPLICATION NUMBER: US 60/008,233
; PRIOR FILING DATE: 1995-12-06
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 413
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic polypeptide
US-09-919-703-12

Query Match      100.0%; Score 30; DB 10; Length 413;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 SVDVEY 6
Db      156 SVDVEY 161

RESULT 6
US-09-940-235-2
; Sequence 2, Application US/09940235
; Publication No. US2003005921A1
; GENERAL INFORMATION:
; APPLICANT: Kumar, Rajesh
; APPLICANT: Sahni, Girish
; APPLICANT: Roy, Chaite
; APPLICANT: Rajagopal, Kammara
; APPLICANT: Nihalani, Deepak
; APPLICANT: Sundaram, Vasudha
; APPLICANT: Yadav, Mahavir
; TITLE OF INVENTION: NOVEL CLOT-SPECIFIC STREPTOKINASE
; TITLE OF INVENTION: PROTEINS POSSESSING ALTERED PLASMINOGEN ACTIVATION
; TITLE OF INVENTION: CHARACTERISTICS AND A PROCESS FOR THE PREPARATION OF SAID
; TITLE OF INVENTION: PROTEIN
; FILE REFERENCE: 07064-009002
; CURRENT APPLICATION NUMBER: US/09/940,235
; CURRENT FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 09/471,349
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: IN 3825/DEL/98
; PRIOR FILING DATE: 1998-12-24
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 414
; TYPE: PRT
; ORGANISM: Streptococcus equisimilis
US-09-940-235-2

Query Match      100.0%; Score 30; DB 11; Length 414;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 SVDVEY 6
Db      157 SVDVEY 162

RESULT 7
US-10-300-215-252
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; Sequence 252, Application US/10300215
; Publication No. US20030153043A1
; GENERAL INFORMATION:
; APPLICANT: CARR, Francis Joseph
; APPLICANT: ADAIR, Fiona Suzanne
; APPLICANT: HAMILTON, Anita Anne
; APPLICANT: CARTER, Graham
; TITLE OF INVENTION: METHOD FOR THE PRODUCTION OF
; FILE REFERENCE: MER-104-Con.1
; CURRENT APPLICATION NUMBER: US/10/300,215
; CURRENT FILING DATE: 2002-11-20
; PRIOR APPLICATION NUMBER: US 09/438,136
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: WO PCT/GB98/01473
; PRIOR FILING DATE: 1998-05-21
; PRIOR APPLICATION NUMBER: GB 9710480.6
; PRIOR FILING DATE: 1997-05-21
; PRIOR APPLICATION NUMBER: GB 9716197.0
; PRIOR FILING DATE: 1997-07-31
; PRIOR APPLICATION NUMBER: GB 9725270.4
; PRIOR FILING DATE: 1997-11-28
; PRIOR APPLICATION NUMBER: GB 9807751.4
; PRIOR FILING DATE: 1998-04-14
; PRIOR APPLICATION NUMBER: US 60/067,235
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 254
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 252
; LENGTH: 414
; TYPE: PRT
; ORGANISM: Streptococcus equisimilis
US-10-300-215-252

Query Match      100.0%; Score 30; DB 12; Length 414;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 SVDVEY 6
Db      157 SVDVEY 162

RESULT 8
US-10-300-215-253
; Sequence 253, Application US/10300215
; Publication No. US20030153043A1
; GENERAL INFORMATION:
; APPLICANT: CARR, Francis Joseph
; APPLICANT: ADAIR, Fiona Suzanne
; APPLICANT: HAMILTON, Anita Anne
; APPLICANT: CARTER, Graham
; TITLE OF INVENTION: METHOD FOR THE PRODUCTION OF
; FILE REFERENCE: MER-104-Con.1
; CURRENT APPLICATION NUMBER: US/10/300,215
; CURRENT FILING DATE: 2002-11-20
; PRIOR APPLICATION NUMBER: US 09/438,136
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: WO PCT/GB98/01473
; PRIOR FILING DATE: 1998-05-21
; PRIOR APPLICATION NUMBER: GB 9710480.6
; PRIOR FILING DATE: 1997-05-21
; PRIOR APPLICATION NUMBER: GB 9716197.0
; PRIOR FILING DATE: 1997-07-31
; PRIOR APPLICATION NUMBER: GB 9725270.4
; PRIOR FILING DATE: 1997-11-28
; PRIOR APPLICATION NUMBER: GB 9807751.4
; PRIOR FILING DATE: 1998-04-14
; PRIOR APPLICATION NUMBER: US 60/067,235
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 254
; SOFTWARE: FastSeq for Windows Version 4.0
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/ SEQ ID NO 253
/ LENGTH: 414
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Modified strep protein
US-10-300-215-253

Query Match          100.0%; Score 30; DB 12; Length 414;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVDVEY 6
Db 157 SVDVEY 162

RESULT 9
US-09-862-027-25
/ Sequence 25, Application US/09862027
/ Patent No. US20020142428A1
/ GENERAL INFORMATION:
/ APPLICANT: Hodge, Martin R.
/ TITLE OF INVENTION: NO. US20020142428A1el Kinases and Uses Thereof
/ FILE REFERENCE: 35800/234862
/ CURRENT APPLICATION NUMBER: US/09/862,027
/ CURRENT FILING DATE: 2001-05-21
/ PRIOR APPLICATION NUMBER: US 09/345,473
/ PRIOR FILING DATE: 1999-06-30
/ NUMBER OF SEQ ID NOS: 82
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 25
/ LENGTH: 891
/ TYPE: PRT
/ ORGANISM: Hydra vulgaris
US-09-862-027-25

Query Match          100.0%; Score 30; DB 10; Length 891;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVDVEY 6
Db 137 SVDVEY 142

RESULT 10
US-10-369-493-5723
/ Sequence 5723, Application US/10369493
/ Publication No. US20030233675A1
/ GENERAL INFORMATION:
/ APPLICANT: Cao, Yongwei
/ APPLICANT: Hinkle, Gregory J.
/ APPLICANT: Slater, Steven C.
/ APPLICANT: Goldman, Barry S.
/ APPLICANT: Chen, Xianfeng
/ TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
/ FILE REFERENCE: 38-10(52052)B
/ CURRENT APPLICATION NUMBER: US/10/369,493
/ CURRENT FILING DATE: 2003-02-28
/ PRIOR APPLICATION NUMBER: US 60/360,039
/ PRIOR FILING DATE: 2002-02-21
/ NUMBER OF SEQ ID NOS: 47374
/ SEQ ID NO 5723
/ LENGTH: 1207
/ TYPE: PRT
/ ORGANISM: Caenorhabditis elegans
US-10-369-493-5723

Query Match          96.7%; Score 29; DB 12; Length 1207;
Best Local Similarity 83.3%; Pred. No. 5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVDVEY 6
Db 170 SVDVEY 175

RESULT 11
US-10-369-493-6887
/ Sequence 6887, Application US/10369493
/ Publication No. US20030233675A1
/ GENERAL INFORMATION:
/ APPLICANT: Cao, Yongwei
/ APPLICANT: Hinkle, Gregory J.
/ APPLICANT: Slater, Steven C.
/ APPLICANT: Goldman, Barry S.
/ APPLICANT: Chen, Xianfeng
/ TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
/ FILE REFERENCE: 38-10(52052)B
/ CURRENT APPLICATION NUMBER: US/10/369,493
/ CURRENT FILING DATE: 2003-02-28
/ PRIOR APPLICATION NUMBER: US 60/360,039
/ PRIOR FILING DATE: 2002-02-21
/ NUMBER OF SEQ ID NOS: 47374
/ SEQ ID NO 6887
/ LENGTH: 629
/ TYPE: PRT
/ ORGANISM: Caenorhabditis elegans
US-10-369-493-6887

Query Match          93.3%; Score 28; DB 12; Length 629;
Best Local Similarity 66.7%; Pred. No. 4.2e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVDVEY 6
Db 200 SVDVEY 205

RESULT 12
US-09-919-703-3
/ Sequence 3, Application US/09919703
/ Patent No. US20020165129A1
/ GENERAL INFORMATION:
/ APPLICANT: Krystal, Gerald
/ APPLICANT: Rabkin, Simon W.
/ TITLE OF INVENTION: Peptides and Their Use to Ameliorate
/ TITLE OF INVENTION: Cell Death
/ FILE REFERENCE: 50216/003004
/ CURRENT APPLICATION NUMBER: US/09/919,703
/ CURRENT FILING DATE: 2001-07-31
/ PRIOR APPLICATION NUMBER: US 09/294,457
/ PRIOR FILING DATE: 1999-04-19
/ PRIOR APPLICATION NUMBER: US 08/759,599
/ PRIOR FILING DATE: 1996-12-05
/ PRIOR APPLICATION NUMBER: US 60/008,233
/ PRIOR FILING DATE: 1995-12-06
/ NUMBER OF SEQ ID NOS: 16
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 3
/ LENGTH: 6
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Synthetic polypeptide
US-09-919-703-3

Query Match          90.0%; Score 27; DB 10; Length 6;
Best Local Similarity 83.3%; Pred. No. 6.7e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVDVEY 6
Db 200 SVDVEY 205
```

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; TYPE: PRT
; ORGANISM: Gallid herpesvirus 3
US-10-209-967-14

Query Match          90.0%; Score 27; DB 12; Length 391;
Best Local Similarity 83.3%; Pred. No. 4.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 SVDVEY 6
       :|||||
Db      347 SMDVEY 352

RESULT 15
US-10-193-896-12
; Sequence 12, Application US/10193896
; Publication No. US20030129710A1
; GENERAL INFORMATION:
; APPLICANT: Biotechnologisk Institut
; APPLICANT: Jorgensen, Flemming
; APPLICANT: Hansen, Ole C.
; APPLICANT: Stougaard, Peter
; APPLICANT: Berthelsen, Hans
; APPLICANT: Eriknaer, Kristian
; APPLICANT: Botcher, Karen
; APPLICANT: Christensen, Hans Jorgen Singel
; TITLE OF INVENTION: A novel thermostable isomerase and use
; FILE REFERENCE: 30077US02
; CURRENT APPLICATION NUMBER: US/10/193,896
; CURRENT FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/305,155
; PRIOR FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 09/905,108
; PRIOR FILING DATE: 2001-07-16
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 496
; TYPE: PRT
; ORGANISM: T.neapol
US-10-193-896-12

Query Match          90.0%; Score 27; DB 16; Length 496;
Best Local Similarity 83.3%; Pred. No. 5.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 SVDVEY 6
       :|||||
Db      451 AVDVEY 456

RESULT 16
US-09-799-629-14
; Sequence 14, Application US/09799629
; Publication No. US2003008344A1
; GENERAL INFORMATION:
; APPLICANT: ADLER, JON ELLIOT
; APPLICANT: ZOZULYA, SERGEY
; APPLICANT: LI, XIADONG
; APPLICANT: O'CONNELL, SHAWN
; APPLICANT: STASZEWSKI, LENA
; TITLE OF INVENTION: TIR TASTE RECEPTORS AND GENES ENCODING SAME
; FILE REFERENCE: 078003/0277870/RXT
; CURRENT APPLICATION NUMBER: US/09/799,629
; CURRENT FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: 60/187,546
; PRIOR FILING DATE: 2000-03-07
; PRIOR APPLICATION NUMBER: 60/195,536
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 60/209,840
; PRIOR FILING DATE: 2000-06-06
; PRIOR APPLICATION NUMBER: 60/214,213

; TYPE: PRT
; ORGANISM: Gallid herpesvirus 3
US-10-209-967-14

Query Match          90.0%; Score 27; DB 10; Length 355;
Best Local Similarity 83.3%; Pred. No. 3.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 SVDVEY 6
       :|||||
Db      23 TVDVEY 28

RESULT 14
US-10-209-967-14
; Sequence 14, Application US/10209967
; Publication No. US20030171279A1
; GENERAL INFORMATION:
; APPLICANT: MUNGER, JOSHUA
; APPLICANT: ROIZMAN, BERNARD
; TITLE OF INVENTION: METHODS AND COMPOSITION CONCERNING HERPESVIRUS US3 AND
; TITLE OF INVENTION: BAD-INVOLVED APOPTOSIS
; FILE REFERENCE: ARCD:380US
; CURRENT APPLICATION NUMBER: US/10/209,967
; CURRENT FILING DATE: 2002-07-31
; PRIOR APPLICATION NUMBER: 60/308,929
; PRIOR FILING DATE: 2001-07-31
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatenIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 391

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; TYPE: PRT
; ORGANISM: Gallid herpesvirus 3
US-10-209-967-14

Query Match          90.0%; Score 27; DB 12; Length 391;
Best Local Similarity 83.3%; Pred. No. 4.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 SVDVEY 6
       :|||||
Db      347 SMDVEY 352

RESULT 15
US-10-193-896-12
; Sequence 12, Application US/10193896
; Publication No. US20030129710A1
; GENERAL INFORMATION:
; APPLICANT: Biotechnologisk Institut
; APPLICANT: Jorgensen, Flemming
; APPLICANT: Hansen, Ole C.
; APPLICANT: Stougaard, Peter
; APPLICANT: Berthelsen, Hans
; APPLICANT: Eriknaer, Kristian
; APPLICANT: Botcher, Karen
; APPLICANT: Christensen, Hans Jorgen Singel
; TITLE OF INVENTION: A novel thermostable isomerase and use
; FILE REFERENCE: 30077US02
; CURRENT APPLICATION NUMBER: US/10/193,896
; CURRENT FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/305,155
; PRIOR FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 09/905,108
; PRIOR FILING DATE: 2001-07-16
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 496
; TYPE: PRT
; ORGANISM: T.neapol
US-10-193-896-12

Query Match          90.0%; Score 27; DB 16; Length 496;
Best Local Similarity 83.3%; Pred. No. 5.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 SVDVEY 6
       :|||||
Db      451 AVDVEY 456

RESULT 16
US-09-799-629-14
; Sequence 14, Application US/09799629
; Publication No. US2003008344A1
; GENERAL INFORMATION:
; APPLICANT: ADLER, JON ELLIOT
; APPLICANT: ZOZULYA, SERGEY
; APPLICANT: LI, XIADONG
; APPLICANT: O'CONNELL, SHAWN
; APPLICANT: STASZEWSKI, LENA
; TITLE OF INVENTION: TIR TASTE RECEPTORS AND GENES ENCODING SAME
; FILE REFERENCE: 078003/0277870/RXT
; CURRENT APPLICATION NUMBER: US/09/799,629
; CURRENT FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: 60/187,546
; PRIOR FILING DATE: 2000-03-07
; PRIOR APPLICATION NUMBER: 60/195,536
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 60/209,840
; PRIOR FILING DATE: 2000-06-06
; PRIOR APPLICATION NUMBER: 60/214,213

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; TYPE: PRT
; ORGANISM: Gallid herpesvirus 3
US-10-209-967-14

Query Match          90.0%; Score 27; DB 12; Length 391;
Best Local Similarity 83.3%; Pred. No. 4.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 SVDVEY 6
       :|||||
Db      347 SMDVEY 352

RESULT 15
US-10-193-896-12
; Sequence 12, Application US/10193896
; Publication No. US20030129710A1
; GENERAL INFORMATION:
; APPLICANT: Biotechnologisk Institut
; APPLICANT: Jorgensen, Flemming
; APPLICANT: Hansen, Ole C.
; APPLICANT: Stougaard, Peter
; APPLICANT: Berthelsen, Hans
; APPLICANT: Eriknaer, Kristian
; APPLICANT: Botcher, Karen
; APPLICANT: Christensen, Hans Jorgen Singel
; TITLE OF INVENTION: A novel thermostable isomerase and use
; FILE REFERENCE: 30077US02
; CURRENT APPLICATION NUMBER: US/10/193,896
; CURRENT FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/305,155
; PRIOR FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 09/905,108
; PRIOR FILING DATE: 2001-07-16
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 496
; TYPE: PRT
; ORGANISM: T.neapol
US-10-193-896-12

Query Match          90.0%; Score 27; DB 16; Length 496;
Best Local Similarity 83.3%; Pred. No. 5.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 SVDVEY 6
       :|||||
Db      451 AVDVEY 456

RESULT 16
US-09-799-629-14
; Sequence 14, Application US/09799629
; Publication No. US2003008344A1
; GENERAL INFORMATION:
; APPLICANT: ADLER, JON ELLIOT
; APPLICANT: ZOZULYA, SERGEY
; APPLICANT: LI, XIADONG
; APPLICANT: O'CONNELL, SHAWN
; APPLICANT: STASZEWSKI, LENA
; TITLE OF INVENTION: TIR TASTE RECEPTORS AND GENES ENCODING SAME
; FILE REFERENCE: 078003/0277870/RXT
; CURRENT APPLICATION NUMBER: US/09/799,629
; CURRENT FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: 60/187,546
; PRIOR FILING DATE: 2000-03-07
; PRIOR APPLICATION NUMBER: 60/195,536
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 60/209,840
; PRIOR FILING DATE: 2000-06-06
; PRIOR APPLICATION NUMBER: 60/214,213

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; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 60/226,448
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/259,227
; PRIOR FILING DATE: 2001-01-03
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 858
; TYPE: PRT
; ORGANISM: Rattus sp.
US-09-799-629-14

Query Match          90.0%; Score 27; DB 11; Length 858;
Best Local Similarity 83.3%; Pred. No. 9.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 SVDVEY 6
Db      456 SVDMEY 461

RESULT 17
US-09-927-315-25
; Sequence 25, Application US/09927315
; Publication No. US20030040048A1
; GENERAL INFORMATION:
; APPLICANT: Zuker, Charles S.
; APPLICANT: Ryba, Nicholas J. P.
; APPLICANT: Nelson, Greg
; APPLICANT: Hoon, Mark A.
; APPLICANT: Chandrasekar, Jayaram
; APPLICANT: Zhang, Yifeng
; APPLICANT: The Regents of the University of California
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by the Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Mammalian Sweet Taste Receptors
; FILE REFERENCE: 02307E-120110US
; CURRENT APPLICATION NUMBER: US/09/927,315
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: US 60/302,898
; PRIOR FILING DATE: 2001-07-03
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 858
; TYPE: PRT
; ORGANISM: Rattus sp.
; FEATURE:
; OTHER INFORMATION: rat Tir3 sweet taste receptor
US-09-927-315-25

Query Match          90.0%; Score 27; DB 11; Length 858;
Best Local Similarity 83.3%; Pred. No. 9.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 SVDVEY 6
Db      456 SVDMEY 461

RESULT 18
US-10-246-785-9
; Sequence 9, Application US/10246785
; Publication No. US2003014848A1
; GENERAL INFORMATION:
; APPLICANT: IRM, LLC
; APPLICANT: The Scripps Research Institute
; APPLICANT: Liao, Jiayu
; APPLICANT: Sheng, Ding
; APPLICANT: Schuitz, Peter G
; TITLE OF INVENTION: Sweet Taste Receptors
; APPLICANT: ZOLLER, MARK

US-10-179-373-4
; Sequence 4, Application US/10179373
; Publication No. US2003023407A1
; GENERAL INFORMATION:
; APPLICANT: ZOLLER, MARK

US-10-190-417-25
; Sequence 25, Application US/10190417
; Publication No. US20030166137A1
; GENERAL INFORMATION:
; APPLICANT: Zuker, Charles S.
; APPLICANT: Ryba, Nicholas J. P.
; APPLICANT: Chandrasekar, Jayaram
; APPLICANT: Hoon, Mark A.
; APPLICANT: Nelson, Greg
; APPLICANT: Zhang, Yifeng
; APPLICANT: The Regents of the University of California
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by the Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Mammalian Sweet and Amino Acid Heterodimeric Taste
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: 02307E-120130US
; CURRENT APPLICATION NUMBER: US/10/190,417
; CURRENT FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: US 60/302,898
; PRIOR FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: US 09/927,315
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: US 60/358,925
; PRIOR FILING DATE: 2002-02-22
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 858
; TYPE: PRT
; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: rat Tir3
US-10-190-417-25

Query Match          90.0%; Score 27; DB 12; Length 858;
Best Local Similarity 83.3%; Pred. No. 9.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 SVDVEY 6
Db      456 SVDMEY 461

RESULT 20
US-10-179-373-4
; Sequence 4, Application US/10179373
; Publication No. US2003023407A1
; GENERAL INFORMATION:
; APPLICANT: ZOLLER, MARK
```



APPLICANT: LI, XIAODONG  
APPLICANT: STASZEWski, LENA  
APPLICANT: O'CONNELL, SHAWN  
APPLICANT: ZOZULYA, SERGEY  
APPLICANT: ADLER, JON  
APPLICANT: XU, HONG  
APPLICANT: ECHEVERRI, FERNANDO  
TITLE OF INVENTION: T1R HETERO-OLIGOMERIC TASTE RECEPTORS AND CELL LINES  
TITLE OF INVENTION: THAT EXPRESS SAID RECEPTORS AND USE THEREOF FOR  
TITLE OF INVENTION: IDENTIFICATION OF TASTE COMPOUNDS  
FILE REFERENCE: 078003-0291566  
CURRENT APPLICATION NUMBER: US/10/179,373  
CURRENT FILING DATE: 2002-06-26  
PRIOR APPLICATION NUMBER: 60/300,434  
PRIOR FILING DATE: 2001-06-26  
PRIOR APPLICATION NUMBER: 60/304,749  
PRIOR FILING DATE: 2001-07-13  
PRIOR APPLICATION NUMBER: 60/310,493  
PRIOR FILING DATE: 2001-08-08  
PRIOR APPLICATION NUMBER: 60/331,771  
PRIOR FILING DATE: 2001-11-21  
PRIOR APPLICATION NUMBER: 60/339,472  
PRIOR FILING DATE: 2001-12-14  
PRIOR APPLICATION NUMBER: 60/372,090  
PRIOR FILING DATE: 2002-04-15  
PRIOR APPLICATION NUMBER: 60/374,143  
PRIOR FILING DATE: 2002-04-22  
NUMBER OF SEQ ID NOS: 19  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 4  
LENGTH: 858  
TYPE: PRT  
ORGANISM: Rattus sp.  
US-10-179-373-4

Query Match 90.0%; Score 27; DB 12; Length 858;  
Best Local Similarity 83.3%; Pred. No. 9.8e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVEY 6  
DB 456 SVDMEY 461

RESULT 21  
US-10-035-045-14  
Sequence 14; Application US/10035045  
Publication No. US20030054448A1  
GENERAL INFORMATION:  
APPLICANT: ADLER, JON ELLIOT  
APPLICANT: LI, XIAODONG  
APPLICANT: STASZEWski, LENA  
APPLICANT: O'CONNELL, SHAWN  
APPLICANT: ZOZULYA, SERGEY  
TITLE OF INVENTION: T1R TASTE RECEPTORS AND GENES ENCODING SAME  
FILE REFERENCE: 078003-0280681  
CURRENT APPLICATION NUMBER: US/10/035,045  
CURRENT FILING DATE: 2002-01-03  
PRIOR APPLICATION NUMBER: 60/259,227  
PRIOR FILING DATE: 2001-01-03  
PRIOR APPLICATION NUMBER: 60/284,547  
PRIOR FILING DATE: 2001-04-19  
NUMBER OF SEQ ID NOS: 24  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 14  
LENGTH: 858  
TYPE: PRT  
ORGANISM: Rattus sp.  
US-10-035-045-14

Query Match 90.0%; Score 27; DB 15; Length 858;  
Best Local Similarity 83.3%; Pred. No. 9.8e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVEY 6  
DB 456 SVDMEY 461

RESULT 22  
US-10-369-493-1385  
Sequence 1385; Application US/10369493  
Publication No. US20030231675A1  
GENERAL INFORMATION:  
APPLICANT: Cao, Yongwei  
APPLICANT: Hinkle, Gregory J.  
APPLICANT: Slater, Steven C.  
APPLICANT: Goldman, Barry S.  
APPLICANT: Chen, Xianfeng  
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF  
FILE REFERENCE: 38-10(52052)B  
CURRENT APPLICATION NUMBER: US/10/369,493  
CURRENT FILING DATE: 2003-02-28  
PRIOR APPLICATION NUMBER: US 60/360,039  
PRIOR FILING DATE: 2002-02-21  
NUMBER OF SEQ ID NOS: 47374  
SEQ ID NO 1385  
LENGTH: 1471  
TYPE: PRT  
ORGANISM: Saccharomyces cerevisiae  
US-10-369-493-1385

Query Match 90.0%; Score 27; DB 12; Length 1471;  
Best Local Similarity 83.3%; Pred. No. 1.7e+03;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVEY 6  
DB 568 ADVVEY 573

RESULT 23  
US-10-193-477-56  
Sequence 56; Application US/10193477  
Publication No. US20030195163A1  
GENERAL INFORMATION:  
APPLICANT: Bristol-Myers Squibb Company  
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING THREE NOVEL HUMAN CELL SURFACE PROTEINS  
TITLE OF INVENTION: LEUCINE RICH REPEATS AND IMMUNOGLOBULIN FOLDS, BGS2, 3, AND 4,  
TITLE OF INVENTION: THEREOF  
FILE REFERENCE: D0153 NP  
CURRENT APPLICATION NUMBER: US/10/193,477  
CURRENT FILING DATE: 2002-07-11  
PRIOR APPLICATION NUMBER: US 60/304,888  
PRIOR FILING DATE: 2001-07-11  
PRIOR APPLICATION NUMBER: US 60/372,147  
PRIOR FILING DATE: 2002-04-12  
NUMBER OF SEQ ID NOS: 229  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 56  
LENGTH: 18  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-193-477-56

Query Match 86.7%; Score 26; DB 12; Length 18;  
Best Local Similarity 66.7%; Pred. No. 26;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVEY 6  
DB 8 SIDLEY 13

RESULT 24

US-09-737-149-43  
; Sequence 43, Application US/09737149  
; Patent No. US20020077466A1  
; GENERAL INFORMATION:  
; APPLICANT: Spaderna, Steven K  
; APPLICANT: Quinn, Kerry E.  
; APPLICANT: Shimkets, Richard A.  
; APPLICANT: Muralidhara, Padigaru  
; APPLICANT: Spytek, Kimberly A.  
; TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same  
; FILE REFERENCE: 15966-620 CIP  
; CURRENT APPLICATION NUMBER: US/09737,149  
; CURRENT FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: 60/170,564  
; PRIOR FILING DATE: 1999-12-14  
; PRIOR APPLICATION NUMBER: 60/173,165  
; PRIOR FILING DATE: 1999-12-27  
; PRIOR APPLICATION NUMBER: 60/173,362  
; PRIOR FILING DATE: 1999-12-27  
; PRIOR APPLICATION NUMBER: 60/173,544  
; PRIOR FILING DATE: 1999-12-29  
; PRIOR APPLICATION NUMBER: 60/174,404  
; PRIOR FILING DATE: 2000-01-04  
; PRIOR APPLICATION NUMBER: 60/174,962  
; PRIOR FILING DATE: 2000-01-07  
; PRIOR APPLICATION NUMBER: 60/223,929  
; PRIOR FILING DATE: 2000-08-09  
; NUMBER OF SEQ ID NOS: 49  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 43  
; LENGTH: 282  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Consensus Sequence  
; NAME/KEY: VARIANT  
; LOCATION: (1)..(282)  
; OTHER INFORMATION: Where X is a residue at which the query and  
; OTHER INFORMATION: subject sequnces are not identical.  
US-09-737-149-43  
Query Match 86.7%; Score 26; DB 9; Length 282;  
Best Local Similarity 66.7%; Pred. No. 5e+02;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SVDVEY 6  
Db 2 AVDIEY 7  
RESULT 25  
US-09-737-149-42  
; Sequence 42, Application US/09737149  
; Patent No. US20020077466A1  
; GENERAL INFORMATION:  
; APPLICANT: Spaderna, Steven K  
; APPLICANT: Quinn, Kerry E.  
; APPLICANT: Shimkets, Richard A.  
; APPLICANT: Muralidhara, Padigaru  
; APPLICANT: Spytek, Kimberly A.  
; TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same  
; FILE REFERENCE: 15966-620 CIP  
; CURRENT APPLICATION NUMBER: US/09737,149  
; CURRENT FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: 60/170,564  
; PRIOR FILING DATE: 1999-12-14  
; PRIOR APPLICATION NUMBER: 60/173,165  
; PRIOR FILING DATE: 1999-12-27  
; PRIOR APPLICATION NUMBER: 60/173,362  
; PRIOR FILING DATE: 1999-12-27  
; PRIOR APPLICATION NUMBER: 60/173,544  
; PRIOR FILING DATE: 1999-12-29  
; PRIOR APPLICATION NUMBER: 60/174,404  
; PRIOR FILING DATE: 2000-01-04  
; PRIOR APPLICATION NUMBER: 60/174,962  
; PRIOR FILING DATE: 2000-01-07  
; PRIOR APPLICATION NUMBER: 60/223,929  
; PRIOR FILING DATE: 2000-08-09  
; NUMBER OF SEQ ID NOS: 49  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 43  
; LENGTH: 282  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Consensus Sequence  
; NAME/KEY: VARIANT  
; LOCATION: (1)..(282)  
; OTHER INFORMATION: Where X is a residue at which the query and  
; OTHER INFORMATION: subject sequnces are not identical.  
US-09-737-149-43  
Query Match 86.7%; Score 26; DB 9; Length 282;  
Best Local Similarity 66.7%; Pred. No. 5e+02;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SVDVEY 6  
Db 2 AVDIEY 7

US-09-737-149-43  
; PRIOR FILING DATE: 2000-01-04  
; PRIOR APPLICATION NUMBER: 60/174,962  
; PRIOR FILING DATE: 2000-01-07  
; PRIOR APPLICATION NUMBER: 60/223,929  
; PRIOR FILING DATE: 2000-08-09  
; NUMBER OF SEQ ID NOS: 49  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 42  
; LENGTH: 284  
; TYPE: PRT  
; ORGANISM: Rattus norvegicus  
US-09-737-149-42  
Query Match 86.7%; Score 26; DB 9; Length 284;  
Best Local Similarity 66.7%; Pred. No. 5e+02;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SVDVEY 6  
Db 2 AVDIEY 7  
RESULT 26  
US-09-737-149-12  
; Sequence 12, Application US/09737149  
; Patent No. US20020077466A1  
; GENERAL INFORMATION:  
; APPLICANT: Spaderna, Steven K  
; APPLICANT: Quinn, Kerry E.  
; APPLICANT: Shimkets, Richard A.  
; APPLICANT: Muralidhara, Padigaru  
; APPLICANT: Spytek, Kimberly A.  
; TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same  
; FILE REFERENCE: 15966-620 CIP  
; CURRENT APPLICATION NUMBER: US/09737,149  
; CURRENT FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: 60/170,564  
; PRIOR FILING DATE: 1999-12-14  
; PRIOR APPLICATION NUMBER: 60/173,165  
; PRIOR FILING DATE: 1999-12-27  
; PRIOR APPLICATION NUMBER: 60/173,362  
; PRIOR FILING DATE: 1999-12-27  
; PRIOR APPLICATION NUMBER: 60/173,544  
; PRIOR FILING DATE: 1999-12-29  
; PRIOR APPLICATION NUMBER: 60/174,404  
; PRIOR FILING DATE: 2000-01-04  
; PRIOR APPLICATION NUMBER: 60/174,962  
; PRIOR FILING DATE: 2000-01-07  
; PRIOR APPLICATION NUMBER: 60/223,929  
; PRIOR FILING DATE: 2000-08-09  
; NUMBER OF SEQ ID NOS: 49  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 12  
; LENGTH: 285  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-737-149-12  
Query Match 86.7%; Score 26; DB 9; Length 285;  
Best Local Similarity 66.7%; Pred. No. 5e+02;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SVDVEY 6  
Db 3 AVDIEY 8  
RESULT 27  
US-10-369-493-16538  
; Sequence 16538, Application US/10369493  
; Publication No. US20030233675A1  
; GENERAL INFORMATION:  
; APPLICANT: Cao, Yongwei

; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Chen, Xianfeng  
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF  
; FILE REFERENCE: 38-10(52052)B  
; CURRENT APPLICATION NUMBER: US/10/369,493  
; PRIOR FILING DATE: 2003-02-28  
; PRIOR APPLICATION NUMBER: US 60/360,039  
; PRIOR FILING DATE: 2002-02-21  
; NUMBER OF SEQ ID NOS: 47374  
; SEQ ID NO 16538  
; LENGTH: 287  
; TYPE: PRT  
; ORGANISM: Bacillus thuringiensis  
US-10-369-493-16538

Query Match 86.7%; Score 26; DB 12; Length 287;  
Best Local Similarity 100.0%; Pred. No. 5.1e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDVEY 6  
| | | | |  
Db 31 VDVEY 35

RESULT 28  
US-10-369-493-22955  
; Sequence 22955, Application US/10369493  
; Publication No. US20030233675A1  
; GENERAL INFORMATION:  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Chen, Xianfeng  
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF  
; FILE REFERENCE: 38-10(52052)B  
; CURRENT APPLICATION NUMBER: US/10/369,493  
; CURRENT FILING DATE: 2003-02-28  
; PRIOR FILING DATE: 2003-02-28  
; PRIOR APPLICATION NUMBER: US 60/360,039  
; PRIOR FILING DATE: 2002-02-21  
; NUMBER OF SEQ ID NOS: 47374  
; SEQ ID NO 22955  
; LENGTH: 305  
; TYPE: PRT  
; ORGANISM: Aeropyrum pernix  
US-10-369-493-22955

Query Match 86.7%; Score 26; DB 12; Length 305;  
Best Local Similarity 100.0%; Pred. No. 5.4e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDVEY 6  
| | | | |  
Db 177 VDVEY 181

RESULT 29  
US-10-369-493-19042  
; Sequence 19042, Application US/10369493  
; Publication No. US20030233675A1  
; GENERAL INFORMATION:  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Chen, Xianfeng  
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF  
; FILE REFERENCE: 38-10(52052)B

; CURRENT APPLICATION NUMBER: US/10/369,493  
; CURRENT FILING DATE: 2003-02-28  
; PRIOR APPLICATION NUMBER: US 60/360,039  
; PRIOR FILING DATE: 2002-02-21  
; NUMBER OF SEQ ID NOS: 47374  
; SEQ ID NO 19042  
; LENGTH: 322  
; TYPE: PRT  
; ORGANISM: Anabaena PCC7120  
US-10-369-493-19042

Query Match 86.7%; Score 26; DB 12; Length 322;  
Best Local Similarity 100.0%; Pred. No. 5.7e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VDVEY 6  
| | | | |  
Db 192 VDVEY 196

RESULT 30  
US-10-156-761-12808  
; Sequence 12808, Application US/10156761  
; Publication No. US20030119018A1  
; GENERAL INFORMATION:  
; APPLICANT: OMURA, SATOSHI  
; APPLICANT: IKEDA, HARUO  
; APPLICANT: ISHIKAWA, JUN  
; APPLICANT: HORIKAWA, HIROSHI  
; APPLICANT: SHIBA, TADAYOSHI  
; APPLICANT: SAKAKI, YOSHIYUKI  
; APPLICANT: HATTORI, MASAHIRA  
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES  
; FILE REFERENCE: 249-262  
; CURRENT APPLICATION NUMBER: US/10/156,761  
; CURRENT FILING DATE: 2002-05-29  
; PRIOR APPLICATION NUMBER: JP 2001-204089  
; PRIOR FILING DATE: 2001-05-30  
; PRIOR APPLICATION NUMBER: JP 2001-272697  
; PRIOR FILING DATE: 2001-08-02  
; NUMBER OF SEQ ID NOS: 15109  
; SEQ ID NO 12808  
; LENGTH: 349  
; TYPE: PRT  
; ORGANISM: Streptomyces avermitilis  
US-10-156-761-12808

Query Match 86.7%; Score 26; DB 15; Length 349;  
Best Local Similarity 66.7%; Pred. No. 6.2e+02;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 VDVEY 6  
| : | | |  
Db 243 SIDLEY 248

RESULT 31  
US-10-289-762-1049  
; Sequence 1049, Application US/10289762  
; Publication No. US20040006218A1  
; GENERAL INFORMATION:  
; APPLICANT: Griffais, R.  
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragment  
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prev  
; TITLE OF INVENTION: and treatment of infection  
; FILE REFERENCE: 9710-003-999  
; CURRENT APPLICATION NUMBER: US/10/289,762  
; CURRENT FILING DATE: 2003-03-27  
; NUMBER OF SEQ ID NOS: 6849  
; SEQ ID NO 1049  
; LENGTH: 358  
; TYPE: PRT  
; ORGANISM: Chlamydia pneumoniae

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US-10-289-762-1049
Query Match      86.7%; Score 26; DB 12; Length 358;
Best Local Similarity 100.0%; Pred. No. 6.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VDVEY 6
Db 148 VDVEY 152
|||||

RESULT 32
US-10-369-493-1147
; Sequence 1147, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: CAO, YONGWEI
; APPLICANT: HINKLE, GREGORY J.
; APPLICANT: SLATER, STEVEN C.
; APPLICANT: GOLDMAN, BARRY S.
; APPLICANT: CHEN, XIANFENG
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 1147
; LENGTH: 395
; TYPE: PRT
; ORGANISM: Methanobacterium thermoautotrophicum
US-10-369-493-1147

Query Match      86.7%; Score 26; DB 12; Length 395;
Best Local Similarity 100.0%; Pred. No. 7.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VDVEY 6
Db 84 VDVEY 88
|||||

RESULT 33
US-10-369-493-13245
; Sequence 13245, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: CAO, YONGWEI
; APPLICANT: HINKLE, GREGORY J.
; APPLICANT: SLATER, STEVEN C.
; APPLICANT: GOLDMAN, BARRY S.
; APPLICANT: CHEN, XIANFENG
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 13245
; LENGTH: 410
; TYPE: PRT
; ORGANISM: Aspergillus nidulans
US-10-369-493-13245

Query Match      86.7%; Score 26; DB 12; Length 410;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VDVEY 6

US-10-289-762-1049
Query Match      86.7%; Score 26; DB 12; Length 358;
Best Local Similarity 100.0%; Pred. No. 6.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VDVEY 6
Db 148 VDVEY 152
|||||

RESULT 32
US-10-369-493-1147
; Sequence 1147, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: CAO, YONGWEI
; APPLICANT: HINKLE, GREGORY J.
; APPLICANT: SLATER, STEVEN C.
; APPLICANT: GOLDMAN, BARRY S.
; APPLICANT: CHEN, XIANFENG
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 1147
; LENGTH: 395
; TYPE: PRT
; ORGANISM: Methanobacterium thermoautotrophicum
US-10-369-493-1147

Query Match      86.7%; Score 26; DB 12; Length 395;
Best Local Similarity 100.0%; Pred. No. 7.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VDVEY 6
Db 84 VDVEY 88
|||||

RESULT 33
US-10-369-493-13245
; Sequence 13245, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: CAO, YONGWEI
; APPLICANT: HINKLE, GREGORY J.
; APPLICANT: SLATER, STEVEN C.
; APPLICANT: GOLDMAN, BARRY S.
; APPLICANT: CHEN, XIANFENG
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 13245
; LENGTH: 410
; TYPE: PRT
; ORGANISM: Aspergillus nidulans
US-10-369-493-13245

Query Match      86.7%; Score 26; DB 12; Length 410;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VDVEY 6

US-09-738-626-5998
Query Match      86.7%; Score 26; DB 10; Length 461;
Best Local Similarity 66.7%; Pred. No. 8.4e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVDVEY 6
Db 266 TVDIEY 271
|||||

RESULT 34
US-09-738-626-5998
; Sequence 5998, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: Patent in ver. 3.0
; SEQ ID NO 5998
; LENGTH: 461
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-5998

Query Match      86.7%; Score 26; DB 10; Length 461;
Best Local Similarity 66.7%; Pred. No. 8.4e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVDVEY 6
Db 266 TVDIEY 271
|||||

RESULT 35
US-10-369-493-2914
; Sequence 2914, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: CAO, YONGWEI
; APPLICANT: HINKLE, GREGORY J.
; APPLICANT: SLATER, STEVEN C.
; APPLICANT: GOLDMAN, BARRY S.
; APPLICANT: CHEN, XIANFENG
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 2914
; LENGTH: 496
; TYPE: PRT
; ORGANISM: Thermotoga maritima
US-10-369-493-2914

Query Match      86.7%; Score 26; DB 12; Length 496;
Best Local Similarity 66.7%; Pred. No. 9.1e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
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QY      1 SVDVEY 6
      :|||||
Db      451 AIDVEY 456

RESULT 36
US-10-193-896-11
; Sequence 11, Application US/10193896
; Publication No. US20030129710A1
; GENERAL INFORMATION:
; APPLICANT: Biologisk Institut
; APPLICANT: Jorgensen, Flemming
; APPLICANT: Hansen, Ole C.
; APPLICANT: Stougaard, Peter
; APPLICANT: Berthelsen, Hans
; APPLICANT: Eriksner, Kristian
; APPLICANT: Bottcher, Karen
; APPLICANT: Christensen, Hans Jorgen Singel
; TITLE OF INVENTION: A novel thermostable isomerase and use
; FILE REFERENCE: 30077US02
; CURRENT APPLICATION NUMBER: US/10/193,896
; CURRENT FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/305,155
; PRIOR FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 09/905,108
; PRIOR FILING DATE: 2001-07-16
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 496
; TYPE: PRT
; ORGANISM: T.maritima
US-10-193-896-11

Query Match      86.7%; Score 26; DB 16; Length 496;
Best Local Similarity 66.7%; Pred. No. 9.1e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 SVDVEY 6
      :|||||
Db      451 AIDVEY 456

RESULT 37
US-10-121-032-21
; Sequence 21, Application US/10121032
; Publication No. US2002015550A1
; GENERAL INFORMATION:
; APPLICANT: Bylina, Edward J.
; TITLE OF INVENTION: GLYCOSIDASE ENZYMES
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Gray Cary Ware & Freidenrich LLP
; STREET: 4365 Executive Drive, Suite 1600
; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/121,032
; FILING DATE: 09-Apr-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/134,078
; FILING DATE: 13-AUG-1998
; APPLICATION NUMBER: 08/949,026
```

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; FILING DATE: 10-OCT-1997
; APPLICATION NUMBER: 60/056,916
; FILING DATE: 06-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 09010/024002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 858/677-1456
; TELEFAX: 858/677-1465
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 511 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; SEQUENCE DESCRIPTION: SEQ ID NO: 21:
US-10-121-032-21

Query Match      86.7%; Score 26; DB 14; Length 511;
Best Local Similarity 100.0%; Pred. No. 9.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 VDVVEY 6
      :|||||
Db      95 VDVVEY 99

RESULT 38
US-10-093-037-21
; Sequence 21, Application US/10093037
; Publication No. US20030078397A1
; GENERAL INFORMATION:
; APPLICANT: Jay M. Short
; APPLICANT: Bylina, Edward
; APPLICANT: Swanson, Ronald V.
; APPLICANT: Mathur, Eric J.
; APPLICANT: Lam, David E.
; TITLE OF INVENTION: ENZYMES HAVING GLYCOSIDASE ACTIVITY AND METHODS OF USE THEREOF
; FILE REFERENCE: 09010-024006
; CURRENT APPLICATION NUMBER: US/10/093,037
; CURRENT FILING DATE: 2002-03-06
; PRIOR APPLICATION NUMBER: US 09/910,579
; PRIOR FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 09/134,078
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 08/949,026
; PRIOR FILING DATE: 1997-10-10
; PRIOR APPLICATION NUMBER: US 60/056,916
; PRIOR FILING DATE: 1996-12-06
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 511
; TYPE: PRT
; ORGANISM: Thermococcus chitonophagus
US-10-093-037-21

Query Match      86.7%; Score 26; DB 15; Length 511;
Best Local Similarity 100.0%; Pred. No. 9.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 VDVVEY 6
      :|||||
Db      95 VDVVEY 99

RESULT 39
US-10-461-747-2
; Sequence 2, Application US/10461747
; Publication No. US20030232378A1
; GENERAL INFORMATION:
```

APPLICANT: MEHRAN KHODADOUST  
; TITLE OF INVENTION: NOVEL TOLL MOLECULES AND USES THEREOF  
; FILE REFERENCE: MNI-085  
; CURRENT APPLICATION NUMBER: US/10/461,747  
; CURRENT FILING DATE: 2003-06-13  
; PRIOR APPLICATION NUMBER: US/09/586,340  
; PRIOR FILING DATE: 2000-06-02  
; PRIOR APPLICATION NUMBER: 60/137,659  
; PRIOR FILING DATE: 1999-06-04  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 548  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-461-747-2

Query Match 86.7%; Score 26; DB 12; Length 548;  
Best Local Similarity 66.7%; Pred. No. 1.e+03;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVDVEY 6  
|:|:|  
Db 518 SIDLEY 523

RESULT 40  
US-09-815-242-13170  
; Sequence 13170, Application US/09815242  
; Patent No. US20020061569A1  
; GENERAL INFORMATION:  
; APPLICANT: Haselbeck, Robert  
; APPLICANT: Ohlssen, Kari L.  
; APPLICANT: Zyskind, Judith W.  
; APPLICANT: Wall, Daniel  
; APPLICANT: Trawick, John D.  
; APPLICANT: Carr, Grant J.  
; APPLICANT: Yamamoto, Robert T.  
; APPLICANT: Xu, H. Howard  
; TITLE OF INVENTION: Identification of Essential Genes in  
; FILE REFERENCE: ELITRA.011A  
; CURRENT APPLICATION NUMBER: US/09/815,242  
; CURRENT FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/191,078  
; PRIOR FILING DATE: 2000-03-21  
; PRIOR APPLICATION NUMBER: 60/205,848  
; PRIOR FILING DATE: 2000-05-23  
; PRIOR APPLICATION NUMBER: 60/207,727  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: 60/242,578  
; PRIOR FILING DATE: 2000-10-23  
; PRIOR APPLICATION NUMBER: 60/253,625  
; PRIOR FILING DATE: 2000-11-27  
; PRIOR APPLICATION NUMBER: 60/257,931  
; PRIOR FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: 60/269,308  
; PRIOR FILING DATE: 2001-02-16  
; NUMBER OF SEQ ID NOS: 14110  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 13170  
; LENGTH: 572  
; TYPE: PRT  
; ORGANISM: Streptococcus pneumoniae  
US-09-815-242-13170

Query Match 86.7%; Score 26; DB 9; Length 572;  
Best Local Similarity 66.7%; Pred. No. 1.1e+03;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVDVEY 6  
|:|:|  
Db 204 AVDIEX 209

RESULT 41  
US-09-954-342-18  
; Sequence 18, Application US/09954342  
; Publication No. US20030170838A1  
; GENERAL INFORMATION:  
; APPLICANT: MISHRA, VISHNU S.  
; APPLICANT: SPYTEK, KIMBERLY ANN  
; APPLICANT: TAUFIER, RAYMOND J.  
; APPLICANT: VERNET, CORINE A.  
; APPLICANT: COLMAN, STEVEN D.  
; APPLICANT: GORMAN, LINDA  
; APPLICANT: TCHERNEV, VELIZAR T.  
; APPLICANT: MALYANKAR, URIEL M.  
; APPLICANT: SHENOY, SURESH  
; APPLICANT: PADIGARU, MURALIDHARA  
; APPLICANT: GERLACH, VALERIE L.  
; APPLICANT: MACDOUGALL, JOHN R.  
; APPLICANT: SMITHSON, GLENDA  
; APPLICANT: MILLET, ISABELLE  
; APPLICANT: PEYMAN, JOHN  
; APPLICANT: STONE, DAVID  
; APPLICANT: GUNTHER, ERIC  
; APPLICANT: ELLERMAN, KAREN  
; APPLICANT: LI, LI  
; APPLICANT: RASTELLI, LUCA  
; APPLICANT: ZERHUSEN, BRYAN  
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES AND POLYPEPTIDES ENCODED THEREBY  
; FILE REFERENCE: 21402-114  
; CURRENT APPLICATION NUMBER: US/09/954,342  
; CURRENT FILING DATE: 2001-09-17  
; PRIOR APPLICATION NUMBER: 60/233,382  
; PRIOR FILING DATE: 2000-09-18  
; PRIOR APPLICATION NUMBER: 60/240,498  
; PRIOR FILING DATE: 2000-10-13  
; PRIOR APPLICATION NUMBER: 60/260,284  
; PRIOR FILING DATE: 2001-01-08  
; PRIOR APPLICATION NUMBER: 60/260,973  
; PRIOR FILING DATE: 2001-01-11  
; PRIOR APPLICATION NUMBER: 60/264,794  
; PRIOR FILING DATE: 2001-01-29  
; PRIOR APPLICATION NUMBER: 60/238,398  
; PRIOR FILING DATE: 2000-10-06  
; PRIOR APPLICATION NUMBER: 60/232,675  
; PRIOR FILING DATE: 2000-09-15  
; PRIOR APPLICATION NUMBER: 60/274,862  
; PRIOR FILING DATE: 2001-03-09  
; PRIOR APPLICATION NUMBER: 60/233,801  
; PRIOR FILING DATE: 2000-09-19  
; PRIOR APPLICATION NUMBER: 60/232,676  
; PRIOR FILING DATE: 2000-09-15  
; PRIOR APPLICATION NUMBER: 60/233,960  
; PRIOR FILING DATE: 2000-09-20  
; PRIOR APPLICATION NUMBER: 60/233,402  
; PRIOR FILING DATE: 2000-09-18  
; PRIOR APPLICATION NUMBER: 60/233,521  
; PRIOR FILING DATE: 2000-09-19  
; PRIOR APPLICATION NUMBER: 60/233,522  
; PRIOR FILING DATE: 2000-09-19  
; PRIOR APPLICATION NUMBER: 60/232,679  
; PRIOR FILING DATE: 2000-09-15  
; NUMBER OF SEQ ID NOS: 104  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 18  
; LENGTH: 606  
; TYPE: PRT  
; ORGANISM: Unknown Organism  
; FEATURE:  
; OTHER INFORMATION: Description of Unknown Organism: NOVX Polypeptide  
US-09-954-342-18

Query Match 86.7%; Score 26; DB 12; Length 606;

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; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: NOVX Polypeptide
US-09-954-342-20

Query Match      86.7%; Score 26; DB 12; Length 606;
Best Local Similarity 66.7%; Pred. No. 1.1e+03;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVEY 6
Db 576 SIDLEY 581

RESULT 42
US-09-954-342-20
; Sequence 20, Application US/09954342
; Publication No. US20030170838A1
; GENERAL INFORMATION:
; APPLICANT: MISHRA, VISHNU S.
; APPLICANT: SPYTEK, KIMBERLY ANN
; APPLICANT: TAUPIER, RAYMOND J.
; APPLICANT: VERNET, CORINE A.
; APPLICANT: COLMAN, STEVEN D.
; APPLICANT: GORMAN, LINDA
; APPLICANT: TCHERNEV, VELIZAR T.
; APPLICANT: MALYANKAR, URIEL M.
; APPLICANT: SHENOY, SURESH
; APPLICANT: PADIGARU, MURALIDHARA
; APPLICANT: GERLACH, VALERIE L.
; APPLICANT: MACDOUGALL, JOHN R.
; APPLICANT: SMITHSON, GLENDA
; APPLICANT: MILLET, ISABELLE
; APPLICANT: PEYMAN, JOHN
; APPLICANT: STONE, DAVID
; APPLICANT: GUNTHER, ERIK
; APPLICANT: ELLERMAN, KAREN
; APPLICANT: LI, LI
; APPLICANT: RASTELLI, LUCA
; APPLICANT: ZERHUSEN, BRYAN
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES AND POLYPEPTIDES ENCODED THEREBY
; FILE REFERENCE: 21402-114
; CURRENT APPLICATION NUMBER: US/09/954,342
; CURRENT FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: 60/233,382
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: 60/240,498
; PRIOR FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: 60/260,284
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 60/260,973
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: 60/284,794
; PRIOR FILING DATE: 2001-01-29
; PRIOR APPLICATION NUMBER: 60/238,398
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/232,675
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: 60/274,862
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/233,801
; PRIOR FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: 60/232,676
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: 60/233,960
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: 60/233,402
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: 60/233,521
; PRIOR FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: 60/233,522
; PRIOR FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: 60/232,679
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 20
; LENGTH: 606
; TYPE: PRT
;

; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: NOVX Polypeptide
US-09-954-342-20

Query Match      86.7%; Score 26; DB 12; Length 606;
Best Local Similarity 66.7%; Pred. No. 1.1e+03;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVEY 6
Db 576 SIDLEY 581

RESULT 43
US-09-954-342-42
; Sequence 42, Application US/09954342
; Publication No. US20030170838A1
; GENERAL INFORMATION:
; APPLICANT: MISHRA, VISHNU S.
; APPLICANT: SPYTEK, KIMBERLY ANN
; APPLICANT: TAUPIER, RAYMOND J.
; APPLICANT: VERNET, CORINE A.
; APPLICANT: COLMAN, STEVEN D.
; APPLICANT: GORMAN, LINDA
; APPLICANT: TCHERNEV, VELIZAR T.
; APPLICANT: MALYANKAR, URIEL M.
; APPLICANT: SHENOY, SURESH
; APPLICANT: PADIGARU, MURALIDHARA
; APPLICANT: GERLACH, VALERIE L.
; APPLICANT: MACDOUGALL, JOHN R.
; APPLICANT: SMITHSON, GLENDA
; APPLICANT: MILLET, ISABELLE
; APPLICANT: PEYMAN, JOHN
; APPLICANT: STONE, DAVID
; APPLICANT: GUNTHER, ERIK
; APPLICANT: ELLERMAN, KAREN
; APPLICANT: LI, LI
; APPLICANT: RASTELLI, LUCA
; APPLICANT: ZERHUSEN, BRYAN
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES AND POLYPEPTIDES ENCODED THEREBY
; FILE REFERENCE: 21402-114
; CURRENT APPLICATION NUMBER: US/09/954,342
; CURRENT FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: 60/233,382
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: 60/240,498
; PRIOR FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: 60/260,284
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 60/260,973
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: 60/284,794
; PRIOR FILING DATE: 2001-01-29
; PRIOR APPLICATION NUMBER: 60/238,398
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/232,675
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: 60/274,862
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/233,801
; PRIOR FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: 60/232,676
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: 60/233,960
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: 60/233,402
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: 60/233,521
; PRIOR FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: 60/233,522
; PRIOR FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: 60/232,679
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 20
; LENGTH: 606
; TYPE: PRT
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; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 42
; LENGTH: 606
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-954-342-42

Query Match      86.7%; Score 26; DB 12; Length 606;
Best Local Similarity 66.7%; Pred. No. 1.1e+03;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      1 SVDVEY 6
Db      576 SIDLEY 581

RESULT 44
US-10-193-477-4
; Sequence 4, Application US/10193477
; Publication No. US20030195163A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING THREE NOVEL HUMAN CELL SURFACE PROTEINS
; TITLE OF INVENTION: LEUCINE RICH REPEATS AND IMMUNOGLOBULIN FOLDS, BGS2, 3, AND 4,
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: D0153 NP
; CURRENT APPLICATION NUMBER: US/10/193,477
; CURRENT FILING DATE: 2002-07-11
; PRIOR APPLICATION NUMBER: US 60/304,888
; PRIOR FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: US 60/372,147
; PRIOR FILING DATE: 2002-04-12
; NUMBER OF SEQ ID NOS: 229
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 606
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-193-477-4

Query Match      86.7%; Score 26; DB 12; Length 606;
Best Local Similarity 66.7%; Pred. No. 1.1e+03;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      1 SVDVEY 6
Db      576 SIDLEY 581

RESULT 45
US-10-094-749-2513
; Sequence 2513, Application US/10094749
; Publication No. US20030219741A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHICO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTYUKI
; APPLICANT: NAGAHARI, KENJI

US-10-094-749-2513
; Sequence 2513, Application US/10094749
; Publication No. US20030195163A1
; GENERAL INFORMATION:
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: NOVEL FULL-LENGTH cDNA
; FILE REFERENCE: 084335/0160
; CURRENT APPLICATION NUMBER: US/10/094,749
; CURRENT FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 60/350,435
; PRIOR FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: JP 2001-328381
; PRIOR FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 3381
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2513
; LENGTH: 606
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-094-749-2513

Query Match      86.7%; Score 26; DB 12; Length 606;
Best Local Similarity 66.7%; Pred. No. 1.1e+03;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      1 SVDVEY 6
Db      576 SIDLEY 581

RESULT 46
US-10-128-714-3395
; Sequence 3395, Application US/10128714
; Publication No. US20030119013A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Bo
; APPLICANT: Tishkoff, Daniel
; APPLICANT: Zamudio, Carlos
; APPLICANT: Eroshkin, Alexey M
; APPLICANT: Lemieux, Sebastien M
; TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and
; TITLE OF INVENTION: Methods of Use
; FILE REFERENCE: 10182-018-999
; CURRENT APPLICATION NUMBER: US/10/128,714
; CURRENT FILING DATE: 2002-04-23
; PRIOR APPLICATION NUMBER: US 60/285,697
; PRIOR FILING DATE: 2001-04-23
; PRIOR APPLICATION NUMBER: US 60/287,066
; PRIOR FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: US 60/295,890
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/303,899
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: US 60/316,362
; PRIOR FILING DATE: 2001-08-31
; NUMBER OF SEQ ID NOS: 8603
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3395
; LENGTH: 694
; TYPE: PRT
; ORGANISM: Aspergillus fumigatus
US-10-128-714-3395

Query Match      86.7%; Score 26; DB 15; Length 694;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 VDVVEY 6
Db      212 VDVVEY 216

RESULT 47
US-10-128-714-8395
; Sequence 8395, Application US/10128714
; Publication No. US20030119013A1
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; GENERAL INFORMATION:
; APPLICANT: Jiang, Bo
; APPLICANT: Hu, Wengqi
; APPLICANT: Tishkoff, Daniel
; APPLICANT: Zamudio, Carlos
; APPLICANT: Eroshekin, Alexey M
; APPLICANT: Lemieux, Sebastien M
; TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and
; FILE REFERENCE: 10182-018-999
; CURRENT APPLICATION NUMBER: US/10/128,714
; CURRENT FILING DATE: 2002-04-23
; PRIOR APPLICATION NUMBER: US 60/285,697
; PRIOR FILING DATE: 2001-04-23
; PRIOR APPLICATION NUMBER: US 60/287,066
; PRIOR FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: US 60/295,890
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/303,899
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: US 60/316,362
; PRIOR FILING DATE: 2001-08-31
; NUMBER OF SEQ ID NOS: 8603
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 8395
; LENGTH: 694
; TYPE: PRT
; ORGANISM: Aspergillus fumigatus
US-10-128-714-8395

Query Match      86.7%; Score 26; DB 15; Length 694;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 VDVEY 6
DB      212 VDVEY 216

RESULT 48
US-10-369-493-4017
; Sequence 4017, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US/10/369,493
; PRIOR FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 4017
; LENGTH: 725
; TYPE: PRT
; ORGANISM: Neurospora crassa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(725)
; OTHER INFORMATION: unsure at all Xaa locations
US-10-369-493-4017

Query Match      86.7%; Score 26; DB 12; Length 725;
Best Local Similarity 100.0%; Pred. No. 1.4e-03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 VDVEY 6
DB      212 VDVEY 216

RESULT 49
US-10-369-493-22944
; Sequence 22944, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 22944
; LENGTH: 784
; TYPE: PRT
; ORGANISM: Aeropyrum pernix
US-10-369-493-22944

Query Match      86.7%; Score 26; DB 12; Length 784;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 VDVEY 6
DB      739 VDVEY 743

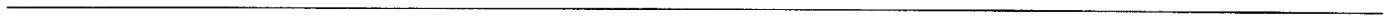
RESULT 50
US-10-291-265-281
; Sequence 281, Application US/10291265
; Publication No. US20030232054A1
; GENERAL INFORMATION:
; APPLICANT: Tang et al
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: No. US20030232054A1el Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-017 (785)
; CURRENT APPLICATION NUMBER: US/10/291,265
; CURRENT FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/617,746
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 09/631,451
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 09/633,870
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 944
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 281
; LENGTH: 968
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-291-265-281

Query Match      86.7%; Score 26; DB 12; Length 968;
Best Local Similarity 83.3%; Pred. No. 1.9e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 SVDVEY 6
DB      283 SVEVEY 288

Search completed: January 20, 2004, 14:02:42
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Job time : 33 secs



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OM protein - protein search, using sw model

Run on: January 20, 2004, 13:54:52 ; Search time 22 Seconds  
(without alignments)  
11.539 Million cell updates/sec

Title: US-09-919-703-1

Perfect score: 30

Sequence: 1 SVDVEY 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 75 summaries

Database :

Issued Patents AA:\*

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2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep.\*

3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep.\*

4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep.\*

5: /cgn2\_6/ptodata/1/iaa/PTUS\_COMB.pep.\*

6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	30	100.0	6	4	US-09-294-457-1
3	30	100.0	16	4	US-09-294-457-5
4	30	100.0	18	2	US-08-759-599-5
5	30	100.0	20	2	US-08-759-599-6
6	30	100.0	20	4	US-09-294-457-6
7	30	100.0	21	2	US-08-759-599-7
8	30	100.0	21	4	US-09-294-457-7
9	30	100.0	150	3	US-09-211-542A-14
10	30	100.0	356	3	US-09-211-542A-12
11	30	100.0	369	1	US-07-854-596B-31
12	30	100.0	372	4	US-09-374-038-3
13	30	100.0	372	4	US-09-658-179-3
14	30	100.0	384	4	US-09-374-038-4
15	30	100.0	384	4	US-09-658-179-4
16	30	100.0	401	4	US-09-374-038-1
17	30	100.0	401	4	US-09-658-179-1
18	30	100.0	413	2	US-08-759-599-12
19	30	100.0	413	4	US-09-374-038-2
20	30	100.0	413	4	US-09-294-457-12
21	30	100.0	413	4	US-09-658-179-2
22	30	100.0	414	3	US-09-211-542A-6
23	30	100.0	414	6	5240845-1
24	30	100.0	415	1	US-07-854-596B-26
25	30	100.0	435	1	US-07-854-596B-19
26	30	100.0	440	1	US-07-854-596B-15
27	30	100.0	440	2	US-08-560-098A-52

#### ALIGNMENTS

#### RESULT 1

US-08-759-599-1

; Sequence 1, Application US/08759599

; Patent No. 5917013

; GENERAL INFORMATION:

; APPLICANT: Rabin, Simon

; APPLICANT: Kyval, Gerald

; TITLE OF INVENTION: NOVEL PEPTIDES AND THEIR USE TO

; TITLE OF INVENTION: AMELIORATE CELL DEATH

; NUMBER OF SEQUENCES: 12

; CORRESPONDENCE ADDRESS:

; ADDRESS: SED and BERRY LLP

; CITY: Seattle

; STATE: Washington

; COUNTRY: US

; ZIP: 98104-7092

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

28	30	100.0	483	1	US-07-854-596B-43	Sequence 43, Appl
29	30	100.0	483	1	US-07-854-596B-47	Sequence 47, Appl
30	30	100.0	499	1	US-07-854-596B-28	Sequence 28, Appl
31	30	100.0	736	3	US-09-211-542A-4	Sequence 4, Appl
32	30	100.0	747	1	US-07-854-596B-40	Sequence 40, Appl
33	30	100.0	795	3	US-09-211-542A-2	Sequence 2, Appl
34	30	100.0	800	2	US-08-488-940-4	Sequence 4, Appl
35	30	100.0	813	2	US-08-488-940-3	Sequence 3, Appl
36	30	100.0	859	1	US-07-854-596B-35	Sequence 35, Appl
37	30	100.0	891	4	US-09-345-473E-25	Sequence 25, Appl
38	30	100.0	1181	2	US-08-488-940-2	Sequence 2, Appl
39	30	100.0	1194	2	US-08-488-940-1	Sequence 1, Appl
40	30	100.0	1194	2	US-08-488-940-17	Sequence 17, Appl
41	30	100.0	1194	2	US-08-488-940-18	Sequence 18, Appl
42	28	93.3	280	4	US-09-470-512A-14	Sequence 14, Appl
43	27	90.0	6	2	US-08-759-599-3	Sequence 3, Appl
44	27	90.0	6	4	US-09-294-457-3	Sequence 3, Appl
45	27	90.0	355	2	US-08-444-646-6	Sequence 6, Appl
46	27	90.0	398	4	US-09-328-352-4507	Sequence 4507, Ap
47	27	90.0	626	4	US-09-328-352-7836	Sequence 7836, Ap
48	27	90.0	885	4	US-09-107-532A-5104	Sequence 5104, Ap
49	26	86.7	12	2	US-08-713-885-3	Sequence 3, Appl
50	26	86.7	71	4	US-09-134-001C-4271	Sequence 4271, Ap
51	26	86.7	199	4	US-09-252-991A-32787	Sequence 32787, A
52	26	86.7	212	4	US-09-252-991A-20153	Sequence 20153, A
53	26	86.7	254	4	US-09-252-991A-17980	Sequence 17980, A
54	26	86.7	284	2	US-08-767-096-3	Sequence 3, Appl
55	26	86.7	284	3	US-09-480-203-3	Sequence 3, Appl
56	26	86.7	326	1	US-08-292-549-4	Sequence 4, Appl
57	26	86.7	326	5	PCT-US91-02207-4	Sequence 4, Appl
58	26	86.7	335	4	US-09-134-001C-5021	Sequence 5021, Ap
59	26	86.7	358	4	US-09-198-452A-1049	Sequence 1049, Ap
60	26	86.7	367	4	US-09-328-352-7523	Sequence 7523, Ap
61	26	86.7	511	4	US-09-134-078-21	Sequence 21, Appl
62	26	86.7	526	2	US-08-698-780A-2	Sequence 2, Appl
63	26	86.7	526	3	US-09-270-917-2	Sequence 2, Appl
64	25	86.7	615	3	US-08-989-299-11	Sequence 11, Appl
65	25	83.3	175	4	US-09-134-001C-4931	Sequence 4931, Ap
66	25	83.3	266	2	US-07-857-224B-39	Sequence 39, Appl
67	25	83.3	430	4	US-09-328-352-5931	Sequence 5931, Ap
68	25	83.3	460	4	US-09-134-001C-5322	Sequence 5322, Ap
69	25	83.3	481	3	US-08-843-659-4	Sequence 4, Appl
70	25	83.3	555	4	US-09-613-872-4	Sequence 4, Appl
71	25	83.3	572	4	US-09-237-111-2	Sequence 2, Appl
72	25	83.3	608	4	US-08-843-572E-2	Sequence 2, Appl
73	25	83.3	761	4	US-09-585-858-28	Sequence 28, Appl
74	25	83.3	789	4	US-09-390-234-16	Sequence 16, Appl
75	24	80.0	15	3	US-08-331-625A-19	Sequence 19, Appl

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/759,599  
FILING DATE: 05-DEC-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: McMasters, David D.  
REGISTRATION NUMBER: 33,963  
REFERENCE/DOCKET NUMBER: 780059.401  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
TELEX: 3723836  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-759-599-1

Query Match 100.0%; Score 30; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVEY 6  
Db 1 SVDVEY 6

RESULT 2  
US-09-294-457-1  
Sequence 1, Application US/09294457  
Patent No. 6348567  
GENERAL INFORMATION:  
APPLICANT: Krystal, Simon W.  
TITLE OF INVENTION: NOVEL PEPTIDES AND THEIR USE TO  
IMPROVE CELL DEATH  
FILE REFERENCE: 50216/003003  
CURRENT APPLICATION NUMBER: US/09/294,457  
PRIOR FILING DATE: 1999-04-19  
PRIOR FILING DATE: 1996-12-05  
PRIOR FILING DATE: 1995-12-06  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 1  
LENGTH: 6  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic polypeptide  
US-09-294-457-1

Query Match 100.0%; Score 30; DB 4; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVEY 6  
Db 1 SVDVEY 6

RESULT 4  
US-08-759-599-5  
Sequence 5, Application US/08759599  
Patent No. 5917013  
GENERAL INFORMATION:  
APPLICANT: Rabkin, Simon  
TITLE OF INVENTION: NOVEL PEPTIDES AND THEIR USE TO  
IMPROVE CELL DEATH  
FILE REFERENCE: 50216/003003  
CURRENT APPLICATION NUMBER: US/08/759,599  
PRIOR FILING DATE: 1999-04-19  
PRIOR FILING DATE: 1996-12-05  
PRIOR FILING DATE: 1995-12-06  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 5  
LENGTH: 16  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic polypeptide  
US-09-294-457-5

Query Match 100.0%; Score 30; DB 2; Length 18;

QY 1 SVDVEY 6  
Db 1 SVDVEY 6

RESULT 3  
US-09-294-457-5  
Sequence 5, Application US/09294457  
Patent No. 6348567  
GENERAL INFORMATION:  
APPLICANT: Krystal, Gerald

Best Local Similarity 100.0%; Pred. No. 1.1;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVDVEY 6  
|||||  
Db 1 SVDVEY 6

RESULT 5  
US-08-759-599-6  
Sequence 6, Application US/08759599  
Patent No. 5917013

GENERAL INFORMATION:  
APPLICANT: Raskin, Simon  
TITLE OF INVENTION: NOVEL PEPTIDES AND THEIR USE TO  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SEED and BERRY LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: US  
ZIP: 98104-7092  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/759,599  
FILING DATE: 05-DEC-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Mcmasters, David D.  
REGISTRATION NUMBER: 33,963  
REFERENCE/DOCKET NUMBER: 780059.401  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
TELEX: 3723836  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-759-599-6

Query Match 100.0%; Score 30; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.3;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVDVEY 6  
|||||  
Db 1 SVDVEY 6

RESULT 6  
US-09-294-457-6  
Sequence 6, Application US/09294457  
Patent No. 6348567  
GENERAL INFORMATION:  
APPLICANT: Kiyatal, Gerald  
TITLE OF INVENTION: No. 6348567el Peptides and Their Use to  
TITLE OF INVENTION: Ameliorate Cell Death  
FILE REFERENCE: 50216/003003  
CURRENT APPLICATION NUMBER: US/09/294,457  
CURRENT FILING DATE: 1999-04-19  
PRIOR APPLICATION NUMBER: US 08/759,599

PRIOR FILING DATE: 1996-12-05  
PRIOR APPLICATION NUMBER: US 60/008,233  
PRIOR FILING DATE: 1995-12-06  
NUMBER OF SEQ ID NOS: 16  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 6  
LENGTH: 20  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic polypeptide  
US-09-294-457-6

Query Match 100.0%; Score 30; DB 4; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.3;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVDVEY 6  
|||||  
Db 1 SVDVEY 6

RESULT 7  
US-08-759-599-7  
Sequence 7, Application US/08759599  
Patent No. 5917013  
GENERAL INFORMATION:  
APPLICANT: Raskin, Simon  
TITLE OF INVENTION: NOVEL PEPTIDES AND THEIR USE TO  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SEED and BERRY LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: US  
ZIP: 98104-7092  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/759,599  
FILING DATE: 05-DEC-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Mcmasters, David D.  
REGISTRATION NUMBER: 33,963  
REFERENCE/DOCKET NUMBER: 780059.401  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
TELEX: 3723836  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 21 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-759-599-7

Query Match 100.0%; Score 30; DB 2; Length 21;  
Best Local Similarity 100.0%; Pred. No. 1.4;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVDVEY 6  
|||||  
Db 1 SVDVEY 6

RESULT 8  
US-09-294-457-7  
Sequence 7, Application US/09294457  
Patent No. 6348567  
GENERAL INFORMATION:  
APPLICANT: Krystal, Gerald  
APPLICANT: Radkin, Simon W.  
TITLE OF INVENTION: No. 6348567el Peptides and Their Use to  
FILE REFERENCE: 50216/003003  
CURRENT APPLICATION NUMBER: US/09/294,457  
CURRENT FILING DATE: 1999-04-19  
PRIOR APPLICATION NUMBER: US 08/759,599  
PRIOR FILING DATE: 1996-12-05  
PRIOR APPLICATION NUMBER: US 60/008,233  
PRIOR FILING DATE: 1995-12-06  
NUMBER OF SEQ ID NOS: 16  
SOFTWARE: FASTSEQ for Windows Version 4.0  
SEQ ID NO 7  
LENGTH: 21  
TYPE: PRP  
ORGANISM: Artificial sequence  
FEATURE:  
OTHER INFORMATION: Synthetic polypeptide  
US-09-294-457-7  
Query Match 100.0%; Score 30; DB 4; Length 21;  
Best Local Similarity 100.0%; Pred. No. 1,4; Mismatches 0; Indels 0; Gaps 0;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SVDVEY 6  
Db 1 SVDVEY 6  
RESULT 9  
US-09-211-542A-14  
Sequence 14, Application US/09211542A  
Patent No. 6210667  
GENERAL INFORMATION:  
APPLICANT: Reed, Guy L.  
TITLE OF INVENTION: BACTERIAL FIBRIN-DEPENDENT PLASMINOGEN ACTIVATOR  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BROMBERG & SUNSTEIN, LLP  
STREET: 125 Summer Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02110  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/211,542A  
FILING DATE: 15-December-1998  
CLASSIFICATION: 1653  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/069,497  
FILING DATE: 15-December-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Attorney, Strimpel, Harriet M.  
REGISTRATION NUMBER: 37,008  
REFERENCE/DOCKET NUMBER: 1874/111  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)443-9292  
TELEFAX: (617)443-0004  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 150 amino acids

TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-211-542A-14  
Query Match 100.0%; Score 30; DB 3; Length 150;  
Best Local Similarity 100.0%; Pred. No. 12; Mismatches 0; Indels 0; Gaps 0;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SVDVEY 6  
Db 14 SVDVEY 19  
RESULT 10  
US-09-211-542A-12  
Sequence 12, Application US/09211542A  
Patent No. 6210667  
GENERAL INFORMATION:  
APPLICANT: Reed, Guy L.  
TITLE OF INVENTION: BACTERIAL FIBRIN-DEPENDENT PLASMINOGEN ACTIVATOR  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BROMBERG & SUNSTEIN, LLP  
STREET: 125 Summer Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02110  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/211,542A  
FILING DATE: 15-December-1998  
CLASSIFICATION: 1653  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/069,497  
FILING DATE: 15-December-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Attorney, Strimpel, Harriet M.  
REGISTRATION NUMBER: 37,008  
REFERENCE/DOCKET NUMBER: 1874/111  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)443-9292  
TELEFAX: (617)443-0004  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 356 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-211-542A-12  
Query Match 100.0%; Score 30; DB 3; Length 356;  
Best Local Similarity 100.0%; Pred. No. 31; Mismatches 0; Indels 0; Gaps 0;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SVDVEY 6  
Db 99 SVDVEY 104  
RESULT 11  
US-07-854-596B-31  
Sequence 31, Application US/07854596B  
Patent No. 5434073  
GENERAL INFORMATION:  
APPLICANT: Dawson, Keith M.  
APPLICANT: Hunter, Michael G.  
APPLICANT: Czaplewski, Lloyd G.

TITLE OF INVENTION: Proteins and nucleic acids  
NUMBER OF SEQUENCES: 73  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dr. John J. McDonnell  
STREET: Ten South Wacker Drive, Suite 3000  
CITY: Chicago  
STATE: IL  
COUNTRY: USA  
ZIP: 60606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/854,596B  
FILING DATE: 03-JUN-1992  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: McDonnell, John J  
REGISTRATION NUMBER: 26,949  
REFERENCE/DOCKET NUMBER: 92,337  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-715-1000  
TELEFAX: 312-715-1234  
TELEX: 910-221-5317  
INFORMATION FOR SEQ ID NO: 31:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 369 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-07-854-596B-31

Query Match 100.0%; Score 30; DB 1; Length 369;  
Best Local Similarity 100.0%; Pred. No. 33;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVEY 6  
|||||  
Db 143 SVDVEY 148

RESULT 12  
US-09-374-038-3  
; Sequence 3, Application US/09374038  
; Patent No. 6309873  
; GENERAL INFORMATION:  
; APPLICANT: Madrazo, Isis Del Carmen Torrens  
; APPLICANT: Garcia, Jose De Jesus De La Fuente  
; APPLICANT: Ojalvo, Ariana Garcia  
; APPLICANT: Menendez, Alina Seraleña  
; APPLICANT: Escalona, Elder Pupo  
; APPLICANT: Masso, Julio Raul Fernandez  
; APPLICANT: Griego, Martha De Jesus Gonzalez  
; TITLE OF INVENTION: STREPTOKINASE MUTANTS  
; FILE REFERENCE: Sequence Listings 1-14 re: 976-5  
; Patent No. 6309873  
; CURRENT APPLICATION NUMBER: US/09/374,038  
; CURRENT FILING DATE: 1999-08-13  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 3  
; LENGTH: 372  
; TYPE: PRT  
; ORGANISM: Streptococcus equisimilis  
US-09-374-038-3

Query Match 100.0%; Score 30; DB 4; Length 372;  
Best Local Similarity 100.0%; Pred. No. 33;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVEY 6

Db 157 SVDVEY 162  
|||||  
RESULT 13  
US-09-658-179-3  
; Sequence 3, Application US/09658179  
; Patent No. 6413759  
; GENERAL INFORMATION:  
; APPLICANT: Madrazo, Isis Del Carmen Torrens  
; APPLICANT: Garcia, Jose De Jesus De La Fuente  
; APPLICANT: Ojalvo, Ariana Garcia  
; APPLICANT: Menendez, Alina Seraleña  
; APPLICANT: Escalona, Elder Pupo  
; APPLICANT: Masso, Julio Raul Fernandez  
; APPLICANT: Griego, Martha De Jesus Gonzalez  
; TITLE OF INVENTION: STREPTOKINASE MUTANTS  
; FILE REFERENCE: Sequence Listings 1-14 re: 976-5  
; Patent No. 6413759  
; CURRENT APPLICATION NUMBER: US/09/658,179  
; CURRENT FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 3  
; LENGTH: 372  
; TYPE: PRT  
; ORGANISM: Streptococcus equisimilis  
US-09-658-179-3

Query Match 100.0%; Score 30; DB 4; Length 372;  
Best Local Similarity 100.0%; Pred. No. 33;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVEY 6  
|||||  
Db 157 SVDVEY 162

RESULT 14  
US-09-374-038-4  
; Sequence 4, Application US/09374038  
; Patent No. 6309873  
; GENERAL INFORMATION:  
; APPLICANT: Madrazo, Isis Del Carmen Torrens  
; APPLICANT: Garcia, Jose De Jesus De La Fuente  
; APPLICANT: Ojalvo, Ariana Garcia  
; APPLICANT: Menendez, Alina Seraleña  
; APPLICANT: Escalona, Elder Pupo  
; APPLICANT: Masso, Julio Raul Fernandez  
; APPLICANT: Griego, Martha De Jesus Gonzalez  
; TITLE OF INVENTION: STREPTOKINASE MUTANTS  
; FILE REFERENCE: Sequence Listings 1-14 re: 976-5  
; Patent No. 6309873  
; CURRENT APPLICATION NUMBER: US/09/374,038  
; CURRENT FILING DATE: 1999-08-13  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 384  
; TYPE: PRT  
; ORGANISM: Streptococcus equisimilis  
US-09-374-038-4

Query Match 100.0%; Score 30; DB 4; Length 384;  
Best Local Similarity 100.0%; Pred. No. 34;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVEY 6  
|||||  
Db 157 SVDVEY 162

RESULT 15

US-09-658-179-4  
; Sequence 4, Application US/09658179  
; Patent No. 6413759  
; GENERAL INFORMATION:  
; APPLICANT: Madrazo, Isis Del Carmen Torrens  
; APPLICANT: Garcia, Jose De Jesus De La Fuente  
; APPLICANT: Ojalvo, Ariana Garcia  
; APPLICANT: Menendez, Alina Seralena  
; APPLICANT: Escalona, Elder Pupo  
; APPLICANT: Masso, Julio Raul Fernandez  
; APPLICANT: Griego, Martha De Jesus Gonzalez  
; TITLE OF INVENTION: STREPTOKINASE MUTANTS  
; FILE REFERENCE: Sequence Listings 1-14 re: 976-5  
; Patent No. 6413759  
; CURRENT APPLICATION NUMBER: US/09/658,179  
; CURRENT FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 384  
; TYPE: PR  
; ORGANISM: Streptococcus equisimilis  
US-09-658-179-4

Query Match 100.0%; Score 30; DB 4; Length 384;  
Best Local Similarity 100.0%; Pred. No. 34;  
Matches 6; Conservative 0; Indels 0; Gaps 0;

QY 1 SYDVEY 6  
Db 157 SYDVEY 162

RESULT 16  
US-09-374-038-1  
; Sequence 1, Application US/09374038  
; Patent No. 6309873  
; GENERAL INFORMATION:  
; APPLICANT: Madrazo, Isis Del Carmen Torrens  
; APPLICANT: Garcia, Jose De Jesus De La Fuente  
; APPLICANT: Ojalvo, Ariana Garcia  
; APPLICANT: Menendez, Alina Seralena  
; APPLICANT: Escalona, Elder Pupo  
; APPLICANT: Masso, Julio Raul Fernandez  
; APPLICANT: Griego, Martha De Jesus Gonzalez  
; TITLE OF INVENTION: STREPTOKINASE MUTANTS  
; FILE REFERENCE: Sequence Listings 1-14 re: 976-5  
; Patent No. 6309873  
; CURRENT APPLICATION NUMBER: US/09/374,038  
; CURRENT FILING DATE: 1999-08-13  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 401  
; TYPE: PR  
; ORGANISM: Streptococcus equisimilis  
US-09-374-038-1

Query Match 100.0%; Score 30; DB 4; Length 401;  
Best Local Similarity 100.0%; Pred. No. 36;  
Matches 6; Conservative 0; Indels 0; Gaps 0;

QY 1 SYDVEY 6  
Db 144 SYDVEY 149

RESULT 17  
US-09-658-179-1  
; Sequence 1, Application US/09658179  
; Patent No. 6413759  
; GENERAL INFORMATION:  
; APPLICANT: Madrazo, Isis Del Carmen Torrens

APPLICANT: Garcia, Jose De Jesus De La Fuente  
; APPLICANT: Ojalvo, Ariana Garcia  
; APPLICANT: Menendez, Alina Seralena  
; APPLICANT: Escalona, Elder Pupo  
; APPLICANT: Masso, Julio Raul Fernandez  
; APPLICANT: Griego, Martha De Jesus Gonzalez  
; TITLE OF INVENTION: STREPTOKINASE MUTANTS  
; FILE REFERENCE: Sequence Listings 1-14 re: 976-5  
; Patent No. 6413759  
; CURRENT APPLICATION NUMBER: US/09/658,179  
; CURRENT FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 401  
; TYPE: PR  
; ORGANISM: Streptococcus equisimilis  
US-09-658-179-1

Query Match 100.0%; Score 30; DB 4; Length 401;  
Best Local Similarity 100.0%; Pred. No. 36;  
Matches 6; Conservative 0; Indels 0; Gaps 0;

QY 1 SYDVEY 6  
Db 144 SYDVEY 149

RESULT 18  
US-08-759-599-12  
; Sequence 12, Application US/08759599  
; Patent No. 5917013  
; GENERAL INFORMATION:  
; APPLICANT: Radkin, Simon  
; APPLICANT: Krystal, Gerald  
; TITLE OF INVENTION: NOVEL PEPTIDES AND THEIR USE TO  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: SEED and BERRY LLP  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: US  
; ZIP: 98104-7092  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/759,599  
; FILING DATE: 05-DEC-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: McMaisters, David D.  
; REGISTRATION NUMBER: 33,963  
; REFERENCE/DOCKET NUMBER: 780059.401  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 622-4900  
; TELEFAX: (206) 682-6031  
; TELEX: 3723836  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 413 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-759-599-12

Query Match 100.0%; Score 30; DB 2; Length 413;  
Best Local Similarity 100.0%; Pred. No. 37;



Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVEY 6  
|||||

Db 156 SVDVEY 161

RESULT 19  
US-09-374-038-2

; Sequence 2, Application US/09374038  
; Patent No. 6309873

; GENERAL INFORMATION:

; APPLICANT: Madrazo, Isis Del Carmen Torrens  
; APPLICANT: Garcia, Jose De Jesus De La Fuente

; APPLICANT: Ojalvo, Ariana Garcia  
; APPLICANT: Menendez, Alina Seraleña

; APPLICANT: Escalona, Elder Pupo  
; APPLICANT: Masso, Julio Raul Fernandez

; APPLICANT: Griego, Martha De Jesus Gonzalez  
; TITLE OF INVENTION: STREPTOKINASE MUTANTS

; FILE REFERENCE: Sequence Listings 1-14 re: 976-5  
; Patent No. 6309873

; CURRENT APPLICATION NUMBER: US/09/374.038  
; CURRENT FILING DATE: 1999-08-13

; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 2  
; LENGTH: 413

; TYPE: PRT  
; ORGANISM: Streptococcus equisimilis

US-09-374-038-2

Query Match 100.0%; Score 30; DB 4; Length 413;  
Best Local Similarity 100.0%; Pred. No. 37;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVEY 6  
|||||

Db 144 SVDVEY 149

RESULT 20  
US-09-294-457-12

; Sequence 12, Application US/09294457  
; Patent No. 6348567

; GENERAL INFORMATION:

; APPLICANT: Krysstal, Gerald  
; APPLICANT: Radkin, Simon W.

; TITLE OF INVENTION: No. 6348567el Peptides and Their Use to  
; FILE REFERENCE: 50216/003003

; CURRENT APPLICATION NUMBER: US/09/294.457  
; CURRENT FILING DATE: 1999-04-19

; PRIOR APPLICATION NUMBER: US 08/759,599  
; PRIOR FILING DATE: 1996-12-05

; PRIOR APPLICATION NUMBER: US 60/008,233  
; PRIOR FILING DATE: 1995-12-06

; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 12  
; LENGTH: 413

; TYPE: PRT  
; ORGANISM: Artificial Sequence

; FEATURE:  
; OTHER INFORMATION: Synthetic polypeptide

US-09-294-457-12

Query Match 100.0%; Score 30; DB 4; Length 413;  
Best Local Similarity 100.0%; Pred. No. 37;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVEY 6  
|||||

Db 156 SVDVEY 161

RESULT 21  
US-09-658-179-2

; Sequence 2, Application US/09658179  
; Patent No. 6413759

; GENERAL INFORMATION:

; APPLICANT: Madrazo, Isis Del Carmen Torrens  
; APPLICANT: Garcia, Jose De Jesus De La Fuente

; APPLICANT: Ojalvo, Ariana Garcia  
; APPLICANT: Menendez, Alina Seraleña

; APPLICANT: Escalona, Elder Pupo  
; APPLICANT: Masso, Julio Raul Fernandez

; APPLICANT: Griego, Martha De Jesus Gonzalez  
; TITLE OF INVENTION: STREPTOKINASE MUTANTS

; FILE REFERENCE: Sequence Listings 1-14 re: 976-5  
; Patent No. 6413759

; CURRENT APPLICATION NUMBER: US/09/658.179  
; CURRENT FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 2  
; LENGTH: 413

; TYPE: PRT  
; ORGANISM: Streptococcus equisimilis

US-09-658-179-2

Query Match 100.0%; Score 30; DB 4; Length 413;  
Best Local Similarity 100.0%; Pred. No. 37;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVEY 6  
|||||

Db 144 SVDVEY 149

RESULT 22  
US-09-211-542A-6

; Sequence 6, Application US/09211542A  
; Patent No. 6210667

; GENERAL INFORMATION:

; APPLICANT: Reed, Guy L.  
; TITLE OF INVENTION: BACTERIAL FIBRIN-DEPENDENT PLASMINOGEN ACTIVATOR

; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: BROMBERG & SUNSTEIN, LLP  
; STREET: 125 Summer Street

; CITY: Boston  
; STATE: Massachusetts

; COUNTRY: USA  
; ZIP: 02110

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/211.542A  
; FILING DATE: 15-December-1998

; CLASSIFICATION: 1653  
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 60/069,497  
; FILING DATE: 15-December-1997

; ATTORNEY/AGENT INFORMATION:  
; NAME: Attorney, Strimpel, Harriet M.

; REGISTRATION NUMBER: 37,008  
; REFERENCE/DOCKET NUMBER: 1874/111

; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617)443-9292

; TELEFAX: (617)443-0004  
; INFORMATION FOR SEQ ID NO: 6:

; SEQUENCE CHARACTERISTICS:

LENGTH: 414 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-211-542A-6

Query Match 100.0%; Score 30; DB 3; Length 414;  
Best Local Similarity 100.0%; Pred. No. 37;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVEY 6  
DB 157 SVDVEY 162

RESULT 23  
5240845-1  
; Patent No. 5240845  
; APPLICANT: FUJII, SETSURO/TAKADA, KAORUKO; KATANO, TAMIKI;  
; MAJIMA, EIJI; OGINO, KOICHI; ONO, KENJI; SAKATA, YASUYO; UENOYAMA,  
; TSUTOMU  
; TITLE OF INVENTION: MUTATED STREPTOKINASE PROTEINS  
; NUMBER OF SEQUENCES: 65  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/549,049  
; FILING DATE: 06-JUL-1990  
; SEQ ID NO:11  
; LENGTH: 414  
5240845-1

Query Match 100.0%; Score 30; DB 6; Length 414;  
Best Local Similarity 100.0%; Pred. No. 37;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVEY 6  
DB 157 SVDVEY 162

RESULT 24  
US-07-854-596B-26  
; Sequence 26, Application US/07854596B  
; Patent No. 5434073  
; GENERAL INFORMATION:  
; APPLICANT: Dawson, Keith M  
; APPLICANT: Hunter, Michael G  
; APPLICANT: Czaplewski, Lloyd G  
; TITLE OF INVENTION: Proteins and nucleic acids  
; NUMBER OF SEQUENCES: 73  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dr. John J. McDonnell  
; STREET: Ten South Wacker Drive, Suite 3000  
; CITY: Chicago  
; STATE: IL  
; COUNTRY: USA  
; ZIP: 60606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/854,596B  
; FILING DATE: 03-JUN-1992  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: McDonnell, John J  
; REGISTRATION NUMBER: 26,949  
; REFERENCE/DOCKET NUMBER: 92,337  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 312-715-1000  
; TELEFAX: 312-715-1234  
; TELEX: 910-221-5317

INFORMATION FOR SEQ ID NO: 26:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 415 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-07-854-596B-26

Query Match 100.0%; Score 30; DB 1; Length 415;  
Best Local Similarity 100.0%; Pred. No. 37;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVEY 6  
DB 158 SVDVEY 163

RESULT 25  
US-07-854-596B-19  
; Sequence 19, Application US/07854596B  
; Patent No. 5434073  
; GENERAL INFORMATION:  
; APPLICANT: Dawson, Keith M  
; APPLICANT: Hunter, Michael G  
; APPLICANT: Czaplewski, Lloyd G  
; TITLE OF INVENTION: Proteins and nucleic acids  
; NUMBER OF SEQUENCES: 73  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dr. John J. McDonnell  
; STREET: Ten South Wacker Drive, Suite 3000  
; CITY: Chicago  
; STATE: IL  
; COUNTRY: USA  
; ZIP: 60606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/854,596B  
; FILING DATE: 03-JUN-1992  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: McDonnell, John J  
; REGISTRATION NUMBER: 26,949  
; REFERENCE/DOCKET NUMBER: 92,337  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 312-715-1000  
; TELEFAX: 312-715-1234  
; TELEX: 910-221-5317  
; INFORMATION FOR SEQ ID NO: 19:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 435 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-07-854-596B-19

Query Match 100.0%; Score 30; DB 1; Length 435;  
Best Local Similarity 100.0%; Pred. No. 39;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVEY 6  
DB 178 SVDVEY 183

RESULT 26  
US-07-854-596B-15  
; Sequence 15, Application US/07854596B  
; Patent No. 5434073  
; GENERAL INFORMATION:

APPLICANT: Dawson, Keith M  
APPLICANT: Hunter, Michael G  
APPLICANT: Czaplowski, Lloyd G  
TITLE OF INVENTION: Proteins and nucleic acids  
NUMBER OF SEQUENCES: 73  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dr. John J. McDonnell  
STREET: Ten South Wacker Drive, Suite 3000  
CITY: Chicago  
STATE: IL  
COUNTRY: USA  
ZIP: 60606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/854,596B  
FILING DATE: 03-JUN-1992  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: McDonnell, John J  
REGISTRATION NUMBER: 26,949  
REFERENCE/DOCKET NUMBER: 92,337  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-715-1000  
TELEFAX: 312-715-1234  
TELEX: 910-221-5317  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 440 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-07-854-596B-15

Query Match 100.0%; Score 30; DB 1; Length 440;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVEY 6  
|||  
Db 183 SVDVEY 188

RESULT 27  
US-08-560-098A-52  
Sequence 52, Application US/08560098A  
Patent No. 5976841  
GENERAL INFORMATION:  
APPLICANT: WENDELT, Stephan  
APPLICANT: HEINZEL-WIELAND, Regina  
APPLICANT: STEFFENS, Gerd Josef  
TITLE OF INVENTION: Proteins having fibrinolytic and  
TITLE OF INVENTION: Coagulation-inhibiting Properties  
NUMBER OF SEQUENCES: 60  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Evenson, McKeown, Edwards & Lenahan  
STREET: 1200 G Street, N.W., Suite 700  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/560,098A  
FILING DATE: 17-NOV-1995  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: P 44 40 892.7  
FILING DATE: 17-NOV-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: EVANS, Joseph D  
REGISTRATION NUMBER: 26,269  
REFERENCE/DOCKET NUMBER: 148/42448  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 628-8800  
TELEFAX: (202) 628-8844  
INFORMATION FOR SEQ ID NO: 52:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 440 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-560-098A-52

Query Match 100.0%; Score 30; DB 2; Length 440;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVEY 6  
|||  
Db 183 SVDVEY 188

RESULT 28  
US-07-854-596B-43  
Sequence 43, Application US/07854596B  
Patent No. 5434073  
GENERAL INFORMATION:  
APPLICANT: Dawson, Keith M  
APPLICANT: Hunter, Michael G  
APPLICANT: Czaplowski, Lloyd G  
TITLE OF INVENTION: Proteins and nucleic acids  
NUMBER OF SEQUENCES: 73  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dr. John J. McDonnell  
STREET: Ten South Wacker Drive, Suite 3000  
CITY: Chicago  
STATE: IL  
COUNTRY: USA  
ZIP: 60606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/854,596B  
FILING DATE: 03-JUN-1992  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: McDonnell, John J  
REGISTRATION NUMBER: 26,949  
REFERENCE/DOCKET NUMBER: 92,337  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-715-1000  
TELEFAX: 312-715-1234  
TELEX: 910-221-5317  
INFORMATION FOR SEQ ID NO: 43:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 483 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-07-854-596B-43

Query Match 100.0%; Score 30; DB 1; Length 483;  
Best Local Similarity 100.0%; Pred. No. 44;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVEY 6  
DB 226 SVDVEY 231

RESULT 29  
US-07-854-596B-47

Sequence 47, Application US/07854596B  
Patent No. 5434073  
GENERAL INFORMATION:  
APPLICANT: Dawson, Keith M  
APPLICANT: Hunter, Michael G  
APPLICANT: Czaplowski, Lloyd G  
TITLE OF INVENTION: Proteins and nucleic acids  
NUMBER OF SEQUENCES: 73  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dr. John J. McDonnell  
STREET: Ten South Wacker Drive, Suite 3000  
CITY: Chicago  
STATE: IL  
COUNTRY: USA  
ZIP: 60606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/854,596B  
FILING DATE: 03-JUN-1992  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: McDonnell, John J  
REGISTRATION NUMBER: 26,949  
REFERENCE/DOCKET NUMBER: 92,337  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-715-1000  
TELEFAX: 312-715-1234  
TELEX: 910-221-5317  
INFORMATION FOR SEQ ID NO: 47:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 483 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-07-854-596B-47

Query Match 100.0%; Score 30; DB 1; Length 483;  
Best Local Similarity 100.0%; Pred. No. 44;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVEY 6  
DB 157 SVDVEY 162

RESULT 30  
US-07-854-596B-28

Sequence 28, Application US/07854596B  
Patent No. 5434073  
GENERAL INFORMATION:  
APPLICANT: Dawson, Keith M  
APPLICANT: Hunter, Michael G  
APPLICANT: Czaplowski, Lloyd G  
TITLE OF INVENTION: Proteins and nucleic acids  
NUMBER OF SEQUENCES: 73  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dr. John J. McDonnell  
STREET: Ten South Wacker Drive, Suite 3000  
CITY: Chicago  
STATE: IL  
COUNTRY: USA  
ZIP: 60606

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/854,596B  
FILING DATE: 03-JUN-1992  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: McDonnell, John J  
REGISTRATION NUMBER: 26,949  
REFERENCE/DOCKET NUMBER: 92,337  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-715-1000  
TELEFAX: 312-715-1234  
TELEX: 910-221-5317  
INFORMATION FOR SEQ ID NO: 28:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 499 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-07-854-596B-28

Query Match 100.0%; Score 30; DB 1; Length 499;  
Best Local Similarity 100.0%; Pred. No. 45;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVEY 6  
DB 242 SVDVEY 247

RESULT 31  
US-09-211-542A-4

Sequence 4, Application US/09211542A  
Patent No. 6210667  
GENERAL INFORMATION:  
APPLICANT: Reed, Guy L.  
TITLE OF INVENTION: BACTERIAL FIBRIN-DEPENDENT PLASMINOGEN ACTIVATOR  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BROMBERG & SUNSTEIN, LLP  
STREET: 125 Summer Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02110  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/211,542A  
FILING DATE: 15-December-1998  
CLASSIFICATION: 1653  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/069,497  
FILING DATE: 15-December-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Attorney, Strimpel, Harriet M.  
REGISTRATION NUMBER: 37,008  
REFERENCE/DOCKET NUMBER: 1874/111  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)443-9292  
TELEFAX: (617)443-0004  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 736 amino acids  
TYPE: amino acid  
TOPOLOGY: linear

MOLECULE TYPE: protein  
US-09-211-542A-4

Query Match 100.0%; Score 30; DB 3; Length 736;  
Best Local Similarity 100.0%; Pred. No. 70;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVEY 6  
Db 479 SVDVEY 484

## RESULT 32

US-07-854-596B-40  
Sequence 40, Application US/07854596B  
Patent No. 5434073  
GENERAL INFORMATION:  
APPLICANT: Dawson, Keith M  
APPLICANT: Hunter, Michael G  
APPLICANT: Czaplewski, Lloyd G  
TITLE OF INVENTION: Proteins and nucleic acids  
NUMBER OF SEQUENCES: 73  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dr. John J. McDonnell  
STREET: Ten South Wacker Drive, Suite 3000  
CITY: Chicago  
STATE: IL  
COUNTRY: USA  
ZIP: 60606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/854,596B  
FILING DATE: 03-JUN-1992  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: McDonnell, John J  
REGISTRATION NUMBER: 26,949  
REFERENCE/DOCKET NUMBER: 92,337  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-715-1000  
TELEFAX: 312-715-1234  
TELEX: 910-221-5317  
INFORMATION FOR SEQ ID NO: 40:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 747 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-07-854-596B-40

Query Match 100.0%; Score 30; DB 1; Length 747;  
Best Local Similarity 100.0%; Pred. No. 71;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVEY 6  
Db 143 SVDVEY 148

## RESULT 33

US-09-211-542A-2  
Sequence 2, Application US/09211542A  
Patent No. 6210667  
GENERAL INFORMATION:  
APPLICANT: Reed, Guy L.  
TITLE OF INVENTION: BACTERIAL FIBRIN-DEPENDENT PLASMINOGEN ACTIVATOR  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BROWBERG & SUNSTEIN, LLP

STREET: 125 Summer Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02110

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/211,542A  
FILING DATE: 15-December-1998  
CLASSIFICATION: 1653

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/069,497  
FILING DATE: 15-December-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Attorney, Stimpel, Harriet M.  
REGISTRATION NUMBER: 37,008  
REFERENCE/DOCKET NUMBER: 1874/111  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)443-9292  
TELEFAX: (617)443-0004  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 795 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-211-542A-2

Query Match 100.0%; Score 30; DB 3; Length 795;  
Best Local Similarity 100.0%; Pred. No. 76;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVEY 6  
Db 538 SVDVEY 543

RESULT 34  
US-08-488-940-4  
Sequence 4, Application US/08488940  
Patent No. 5854049  
GENERAL INFORMATION:

APPLICANT: Reed, Guy L.  
TITLE OF INVENTION: PLASMIN-RESISTANT STREPTOKINASE  
NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02110-2804

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/488,940  
FILING DATE: 09-JUN-1995  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Frazer, Janis K.  
REGISTRATION NUMBER: 34,819  
REFERENCE/DOCKET NUMBER: 05433/009001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617/542-5070  
TELEFAX: 200154

INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 800 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-488-940-4

Query Match 100.0%; Score 30; DB 2; Length 800;  
Best Local Similarity 100.0%; Pred. No. 77;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVEY 6  
Db 143 SVDVEY 148

RESULT 35

US-08-488-940-3  
Sequence 3, Application US/08488940  
Patent No. 5854049

GENERAL INFORMATION:

APPLICANT: Reed, Guy L.  
TITLE OF INVENTION: PLASMIN-RESISTANT STREPTOKINASE  
NUMBER OF SEQUENCES: 20

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA

COUNTRY: USA

ZIP: 02110-2804

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/488,940  
FILING DATE: 09-JUN-1995

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: Fraser, Janis K.  
REGISTRATION NUMBER: 34,819

REFERENCE/DOCKET NUMBER: 05433/009001

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617/542-5070

TELEFAX: 617/542-8906

TELEX: 200154

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 813 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-488-940-3

Query Match 100.0%; Score 30; DB 2; Length 813;  
Best Local Similarity 100.0%; Pred. No. 78;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVEY 6  
Db 156 SVDVEY 161

RESULT 36

US-07-854-596B-35  
Sequence 35, Application US/07854596B  
Patent No. 5434073

GENERAL INFORMATION:

APPLICANT: Dawson, Keith M  
APPLICANT: Hunter, Michael G  
APPLICANT: Czaplinski, Lloyd G  
TITLE OF INVENTION: Proteins and nucleic acids  
NUMBER OF SEQUENCES: 73  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dr. John J. McDonnell  
STREET: Ten South Wacker Drive, Suite 3000  
CITY: Chicago  
STATE: IL

COUNTRY: USA

ZIP: 60606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/854,596B  
FILING DATE: 03-JUN-1992

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: McDonnell, John J

REGISTRATION NUMBER: 26,949

REFERENCE/DOCKET NUMBER: 92,337

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312-715-1000

TELEFAX: 312-715-1234

TELEX: 910-221-5317

INFORMATION FOR SEQ ID NO: 35:

SEQUENCE CHARACTERISTICS:

LENGTH: 859 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-07-854-596B-35

Query Match 100.0%; Score 30; DB 1; Length 859;  
Best Local Similarity 100.0%; Pred. No. 83;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVEY 6  
Db 178 SVDVEY 183

RESULT 37

US-09-345-473E-25  
Sequence 25, Application US/09345473E

Patent No. 6558903

GENERAL INFORMATION:

APPLICANT: Hodge, Martin

TITLE OF INVENTION: No. 6558903el Kinases and Uses Thereof

FILE REFERENCE: 35800/183781

CURRENT APPLICATION NUMBER: US/09/345,473E

NUMBER OF SEQ ID NOS: 62

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 25

LENGTH: 891

TYPE: PRT

ORGANISM: Hydra vulgaris  
US-09-345-473E-25

Query Match 100.0%; Score 30; DB 4; Length 891;  
Best Local Similarity 100.0%; Pred. No. 87;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVEY 6  
Db 137 SVDVEY 142

```
RESULT 38
US-08-488-940-2
; Sequence 2, Application US/08488940
; Patent No. 5854049
; GENERAL INFORMATION:
; APPLICANT: Reed, Guy L.
; TITLE OF INVENTION: PLASMIN-RESISTANT STREPTOKINASE
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,940
; FILING DATE: 09-JUN-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 05433/009001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEEX: 200154
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1181 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
US-08-488-940-2

Query Match          100.0%; Score 30; DB 2; Length 1181;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SVDVEY 6
Db      524 SVDVEY 529

RESULT 39
US-08-488-940-1
; Sequence 1, Application US/08488940
; Patent No. 5854049
; GENERAL INFORMATION:
; APPLICANT: Reed, Guy L.
; TITLE OF INVENTION: PLASMIN-RESISTANT STREPTOKINASE
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,940
; FILING DATE: 09-JUN-1995
```

```
CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 05433/009001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEEX: 200154
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1194 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
US-08-488-940-1

Query Match          100.0%; Score 30; DB 2; Length 1194;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SVDVEY 6
Db      537 SVDVEY 542

RESULT 40
US-08-488-940-17
; Sequence 17, Application US/08488940
; Patent No. 5854049
; GENERAL INFORMATION:
; APPLICANT: Reed, Guy L.
; TITLE OF INVENTION: PLASMIN-RESISTANT STREPTOKINASE
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,940
; FILING DATE: 09-JUN-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 05433/009001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEEX: 200154
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1194 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
US-08-488-940-17

Query Match          100.0%; Score 30; DB 2; Length 1194;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SVDVEY 6
```

Db 537 SYDVEY 542

RESULT 41  
US-08-488-940-18

Sequence 18, Application US/08488940  
Patent No. 5854049

GENERAL INFORMATION:

APPLICANT: Reed, Guy L.

TITLE OF INVENTION: PLASMIN-RESISTANT STREPTOKINASE

NUMBER OF SEQUENCES: 20

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson P.C.

STREET: 225 Franklin Street

CITY: Boston

STATE: MA

COUNTRY: USA

ZIP: 02110-2804

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/488,940

FILING DATE: 09-JUN-1995

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: Fraser, Janis K.

REGISTRATION NUMBER: 34,819

REFERENCE/DOCKET NUMBER: 05433/009001

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617/542-5070

TELEFAX: 617/542-8906

TELEX: 200154

INFORMATION FOR SEQ ID NO: 18:

SEQUENCE CHARACTERISTICS:

LENGTH: 1194 amino acids

TYPE: amino acid

STRANDEDNESS: not relevant

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-488-940-18

Query Match

Best Local Similarity 100.0%; Score 30; DB 2; Length 1194;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYDVEY 6

Db 537 SYDVEY 542

RESULT 42

US-09-470-512A-14

Sequence 14, Application US/09470512A

Patent No. 6376652

GENERAL INFORMATION:

APPLICANT: PhageTech, Inc.

TITLE OF INVENTION: Compositions and methods involving an essential Staphylococcus Au

FILE REFERENCE: 21715/1000

CURRENT APPLICATION NUMBER: US/09/470,512A

CURRENT FILING DATE: 1999-12-12

NUMBER OF SEQ ID NOS: 16

SOFTWARE: Patentin version 3.0

SEQ ID NO 14

LENGTH: 280

TYPE: PRT

ORGANISM: Bacillus subtilis

US-09-470-512A-14

Query Match 93.3%; Score 28; DB 4; Length 280;  
Best Local Similarity 66.7%; Pred. No. 68;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYDVEY 6  
Db 63 SIDIEY 68

RESULT 43

US-08-759-599-3

Sequence 3, Application US/08759599

Patent No. 5917013

GENERAL INFORMATION:

APPLICANT: Radkin, Simon

APPLICANT: Krystal, Gerald

TITLE OF INVENTION: NOVEL PEPTIDES AND THEIR USE TO

TITLE OF INVENTION: AMELIORATE CELL DEATH

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSEE: SEED and BERRY LLP

STREET: 6300 Columbia Center, 701 Fifth Avenue

CITY: Seattle

STATE: Washington

COUNTRY: US

ZIP: 98104-7092

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/759,599

FILING DATE: 05-DEC-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: McMaister, David D.

REGISTRATION NUMBER: 33,963

REFERENCE/DOCKET NUMBER: 780059.401

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 622-4900

TELEFAX: (206) 682-6031

TELEX: 3723836

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 6 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-759-599-3

Query Match

Best Local Similarity 83.3%; Score 27; DB 2; Length 6;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYDVEY 6

Db 1 TVDVEY 6

RESULT 44

US-09-294-457-3

Sequence 3, Application US/09294457

Patent No. 6348567

GENERAL INFORMATION:

APPLICANT: Krystal, Gerald

APPLICANT: Radkin, Simon W

TITLE OF INVENTION: NO. 6348567el Peptides and Their Use to

TITLE OF INVENTION: Ameliorate Cell Death

FILE REFERENCE: 50216/003003

CURRENT APPLICATION NUMBER: US/09/294,457

CURRENT FILING DATE: 1999-04-19



PRIOR APPLICATION NUMBER: US 08/759,599  
PRIOR FILING DATE: 1996-12-05  
PRIOR APPLICATION NUMBER: US 60/008,233  
PRIOR FILING DATE: 1995-12-06  
NUMBER OF SEQ ID NOS: 16  
SOFTWARE: FASTSEQ for Windows Version 4.0  
SEQ ID NO 3  
LENGTH: 6  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic polypeptide  
US-09-294-457-3

Query Match 90.0%; Score 27; DB 4; Length 6;  
Best Local Similarity 83.3%; Pred. No. 2.5e+05;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVY 6  
DB 1 TVDVEY 6

RESULT 45  
US-08-444-646-6  
Sequence 6, Application US/08444646  
Patent No. 5837263

GENERAL INFORMATION:  
APPLICANT: Haake, David A.  
APPLICANT: Shang, Ellen S.  
TITLE OF INVENTION: Leptospira MEMBRANE PROTEINS  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Robbins, Berliner & Carson  
STREET: 201 N. Figueroa Street, 5th Floor  
CITY: Los Angeles  
STATE: California  
COUNTRY: USA  
ZIP: 90012-2628  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/444,646  
FILING DATE: 19-MAY-1995  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Wong, Wean Khing  
REGISTRATION NUMBER: 33,561  
REFERENCE/DOCKET NUMBER: 5656-107  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 977-1001  
TELEFAX: (213) 977-1003  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 355 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-444-646-6

Query Match 90.0%; Score 27; DB 2; Length 355;  
Best Local Similarity 83.3%; Pred. No. 1.5e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVY 6  
DB 23 TVDVEY 28

RESULT 46  
US-09-328-352-4507

Sequence 4507, Application US/09328352  
Patent No. 6562958  
GENERAL INFORMATION:  
APPLICANT: Gary L. Breton et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER  
FILE REFERENCE: GTC99-03PA  
CURRENT APPLICATION NUMBER: US/09/328,352  
CURRENT FILING DATE: 1999-06-04  
NUMBER OF SEQ ID NOS: 8252  
SEQ ID NO 4507  
LENGTH: 398  
TYPE: PRT  
ORGANISM: Acinetobacter baumannii  
US-09-328-352-4507

Query Match 90.0%; Score 27; DB 4; Length 398;  
Best Local Similarity 83.3%; Pred. No. 1.7e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVY 6  
DB 270 SVDVY 275

RESULT 47  
US-09-328-352-7836  
Sequence 7836, Application US/09328352  
Patent No. 6562958  
GENERAL INFORMATION:  
APPLICANT: Gary L. Breton et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER  
FILE REFERENCE: GTC99-03PA  
CURRENT APPLICATION NUMBER: US/09/328,352  
CURRENT FILING DATE: 1999-06-04  
NUMBER OF SEQ ID NOS: 8252  
SEQ ID NO 7836  
LENGTH: 626  
TYPE: PRT  
ORGANISM: Acinetobacter baumannii  
US-09-328-352-7836

Query Match 90.0%; Score 27; DB 4; Length 626;  
Best Local Similarity 83.3%; Pred. No. 2.8e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVDVY 6  
DB 230 SVDVY 235

RESULT 48  
US-09-107-532A-5104  
Sequence 5104, Application US/09107532A  
Patent No. 6583275  
GENERAL INFORMATION:  
APPLICANT: Lynn A Doucette-Stamm and David Bush  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO  
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS  
NUMBER OF SEQUENCES: 7310  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: GENOME THERAPEUTICS CORPORATION  
STREET: 100 Beaver Street  
CITY: Waltham  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02354  
COMPUTER READABLE FORM:  
MEDIUM TYPE: CD-ROM ISO9660  
COMPUTER: PC  
OPERATING SYSTEM: <Unknown>  
SOFTWARE: ASCII

```

;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Arinello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 5104:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 885 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEetical: YES
; ORIGINAL SOURCE:
; ORGANISM: Enterococcus faecium
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (B) LOCATION 1..885
; SEQUENCE DESCRIPTION: SEQ ID NO: 5104:
US-09-107-532A-5104

Query Match          90.0%; Score 27; DB 4; Length 885;
Best Local Similarity 83.3%; Pred. No. 4.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 SVDEY 6
Db      517 SVDEY 522

RESULT 49
US-08-713-885-3
; Sequence 3, Application US/08713885
; Patent No. 5985833
; GENERAL INFORMATION:
; APPLICANT: Mosesson, Michael W.
; APPLICANT: Meh, David A.
; TITLE OF INVENTION: THROMBIN INHIBITOR
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Quarles & Brady
; STREET: 411 East Wisconsin Avenue
; CITY: Milwaukee
; STATE: Wisconsin
; COUNTRY: U.S.A.
; ZIP: 53202-4497
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/713,885
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Baker, Jean C.
; REGISTRATION NUMBER: 35,433
; REFERENCE/DOCKET NUMBER: 960296, 93740
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (414) 277-5709
; TELEFAX: (414) 271-3552
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
```

```

;
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-713-885-3

Query Match          86.7%; Score 26; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 5.9;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 VDVEY 6
Db      7 VDVEY 11

RESULT 50
US-09-134-001C-4271
; Sequence 4271, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 4271
; LENGTH: 71
; TYPE: PRN
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-4271

Query Match          86.7%; Score 26; DB 4; Length 71;
Best Local Similarity 66.7%; Pred. No. 42;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 SVDEY 6
Db      36 SVDIDY 41

Search completed: January 20, 2004, 13:58:13
Job time : 23 secs
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